



1/66

```
1  AAAATGTATG GATACAACTT ACGTTTGATG AAAGATTTGG GCTTGAAGAC CCAGAAGATG
   TTTTACATAC CTATGTTGAA TGCAAACTAC TTTCTAAACC CGAACTTCTG GGTCTTCTAC

61  ACATATGCAA GTATGATTTT GTAGAAGTTG AGGAACCCAG TGATGGAAC TATTAGGGC
   TGTATACGTT CATACTAAAA CATCTTCAAC TCCTTGGGTC ACTACCTTGA TATAATCCCC

121 GCTGGTGTGG TTCTGGTACT GTACCAGGAA AACAGATTTC TAAAGGAAAT CAAATTAGGA
   CGACCACACC AAGACCATGA CATGGTCCTT TTGTCTAAAG ATTCCTTTA GTTTAATCCT

+1                               MetAsn IlePheLeu LeuAsnLeuLeu ThrGluGlu ValArgLeu
   ]-----

181 TAAGATTTGT ATCTGATGAA TATTTTCCTT CTGAACCTTC TAACAGAGGA GGTAAGATTA
   ATTCTAAACA TAGACTACTT ATAAAAGGAA GACTTGGAAG ATTGTCTCCT CCATTCTAAT

+1 TyrSerCysThr ProArgAsn PheSerVal SerIleArgGlu GluLeuLys ArgThrAsp
   -----

241 TACAGCTGCA CACCTCGTAA CTTCTCAGTG TCCATAAGGG AAGAACTAAA GAGAACCGAT
   ATGTCGACGT GTGGAGCATT GAAGAGTCAC AGGTATTCCC TTCTTGATTT CTCTTGGCTA

+1 ThrIlePheTrp ProGlyCys LeuLeuVal LysArgCysGly GlyAsnCys AlaCysCys
   -----

301 ACCATTTTCT GGCCAGGTTG TCTCCTGGTT AAACGCTGTG GTGGGAACTG TGCCTGTTGT
   TGGTAAAAGA CCGGTCCAAC AGAGGACCAA TTTGCGACAC CACCCTTGAC ACGGACAACA

+1 LeuHisAsnCys AsnGluCys GlnCysVal ProSerLysVal ThrLysLys TyrHisGlu
   -----

361 CTCCACAATT GCAATGAATG TCAATGTGTC CCAAGCAAAG TTAATAAAAA ATACCACGAG
   GAGGTGTTAA CGTTACTTAC AGTTACACAG GGTTCGTTTC AATGATTTTT TATGGTGCTC

+1 ValLeuGlnLeu ArgProLys ThrGlyVal ArgGlyLeuHis LysSerLeu ThrAspVal
   -----

421 GTCCTTCAGT TGAGACCAAA GACCGGTGTC AGGGGATTGC ACAAATCACT CACCGACGTG
   CAGGAAGTCA ACTCTGGTTT CTGGCCACAG TCCCCTAACG TGTTTAGTGA GTGGCTGCAC

+1 AlaLeuGluHis HisGluGlu CysAspCys ValCysArgGly SerThrGly Gly
   ----->

481 GCCCTGGAGC ACCATGAGGA GTGTGACTGT GTGTGCAGAG GGAGCACAGG AGGATAGCCG
   CGGGACCTCG TGGTACTCCT CACACTGACA CACACGTCTC CCTCGTGTCC TCCTATCGGC

541 CATCACCACC AGCAGCTCTT GCCCAGAGCT GTGCAGTGCA GTGGCTGATT CTATTAGAGA
   GTAGTGGTGG TCGTCGAGAA CGGGTCTCGA CACGTCACGT CACCGACTAA GATAATCTCT

601 ACGTATGCGT TATCTCCATC CTTAATCTCA GTTGTGTTGCT TCAAGGACCT TTCATCTTCA
   TGCATACGCA ATAGAGGTAG GAATTAGAGT CAACAAACGA AGTTCCTGGA AAGTAGAAGT
```

Fig. 1-1



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661	GGATTTACAG	TGCATTCTGA	AAGAGGAGAC	ATCAAACAGA	ATTAGGAGTT	GTGCAACAGC
	CCTAAATGTC	ACGTAAGACT	TTCTCCTCTG	TAGTTTGTCT	TAATCCTCAA	CACGTTGTGC
721	TCTTTTGAGA	GGAGGCCTAA	AGGACAGGAG	AAAAGGTCTT	CAATCGTGGA	AAGAAAATTA
	AGAAAACTCT	CCTCCGGATT	TCCTGTCCTC	TTTTCCAGAA	GTTAGCACCT	TTCTTTTAAT
781	AATGTTGTAT	TAAATAGATC	ACCAGCTAGT	TTCAGAGTTA	CCATGTACGT	ATTCCACTAG
	TTACAACATA	ATTTATCTAG	TGGTCGATCA	AAGTCTCAAT	GGTACATGCA	TAAGGTGATC
841	CTGGGTCTG	TATTTTCAGTT	CTTTCGATAC	GGCTTAGGGT	AATGTCAGTA	CAGGAAAAAA
	GACCCAAGAC	ATAAAGTCAA	GAAAGCTATG	CCGAATCCCA	TTACAGTCAT	GTCCTTTTTT
901	ACTGTGCAAG	TGAGCACCTG	ATTCCGTTGC	CTTGCTTAAC	TCTAAAGCTC	CATGTCCTGG
	TGACACGTTT	ACTCGTGAC	TAAGGCAACG	GAACGAATTG	AGATTTCGAG	GTACAGGACC
961	GCCTAAAATC	GTATAAAATC	TGGATTTTTT	TTTTTTTTTT	TGCTCATATT	CACATATGTA
	CGGATTTTAG	CATATTTTAG	ACCTAAAAAA	AAAAAAAAAA	ACGAGTATAA	GTGTATACAT
1021	AACCAGAACA	TTCTATGTAC	TACAAACCTG	GTTTTTAAAA	AGGAACTATG	TTGCTATGAA
	TTGGTCTTGT	AAGATACATG	ATGTTTGGAC	CAAAAATTTT	TCCTTGATAC	AACGATACTT
1081	TTAAACTTGT	GTCGTGCTGA	TAGGACAGAC	TGGATTTTTT	ATATTTCTTA	TTAAAATTTT
	AATTTGAACA	CAGCACGACT	ATCCTGTCTG	ACCTAAAAAG	TATAAAGAAT	AATTTTAAAG
1141	TGCCATTTAG	AAGAAGAGAA	CTACATTCAT	GGTTTGGAAG	AGATAAACCT	GAAAAGAAGA
	ACGGTAAATC	TTCTTCTCTT	GATGTAAGTA	CCAAACCTTC	TCTATTTGGA	CTTTTCTTCT
1201	GTGGCCTTAT	CTTCACTTTA	TCGATAAGTC	AGTTTATTTG	TTTCATTGTG	TACATTTTTA
	CACCGGAATA	GAAGTGAAAT	AGCTATTGAG	TCAAATAAAC	AAAGTAACAC	ATGTAAAAAT
1261	TATTCTCCTT	TTGACATTAT	AACTGTTGGC	TTTTCTAATC	TTGTAAATA	TATCTATTTT
	ATAAGAGGAA	AACTGTAATA	TTGACAACCG	AAAAGATTAG	AACAATTTAT	ATAGATAAAA
1321	TACCAAAGGT	ATTTAATATT	CTTTTTTATG	ACAACCTAGA	TCAACTATTT	TTAGCTTGGT
	ATGGTTTCCA	TAAATTATAA	GAAAAAATAC	TGTTGAATCT	AGTTGATAAA	AATCGAACCA
1381	AAATTTTTCT	AAACACAATT	GTTATAGCCA	GAGGAACAAA	GATGATATAA	AATATTGTTG
	TTTAAAAAGA	TTTGTGTTAA	CAATATCGGT	CTCCTTGTTT	CTACTATATT	TTATAACAAC
1441	CTCTGACAAA	AATACATGTA	TTTCATTCTC	GTATGGTGCT	AGAGTTAGAT	TAATCTGCAT
	GAGACTGTTT	TTATGTACAT	AAAGTAAGAG	CATACCACGA	TCTCAATCTA	ATTAGACGTA
1501	TTTAAAAAAC	TGAATTGGAA	TAGAATTGGT	AAGTTGCAAA	GACTTTTTGA	AAATAATTAA
	AAATTTTTTG	ACTTAACCTT	ATCTTAACCA	TTCAACGTTT	CTGAAAAACT	TTTATTAATT

Fig. 1-2



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1561 ATTATCATAT CTTCCATTCC TGTTATTGGA GATGAAAATA AAAAGCAACT TATGAAAGTA
TAATAGTATA GAAGGTAAGG ACAATAACCT CTACTTTTAT TTTTCGTTGA ATACTTTCAT

1621 GACATTCAGA TCCAGCCATT ACTAACCTAT TCCTTTTTTG GGGAAATCTG AGCCTAGCTC
CTGTAAAGTCT AGGTCGGTAA TGATTGGATA AGGAAAAAAC CCCTTTAGAC TCGGATCGAG

1681 AGAAAAACAT AAAGCACCTT GAAAAAGACT TGGCAGCTTC CTGATAAAGC GTGCTGTGCT
TCTTTTTGTA TTTCGTGGAA CTTTTTCTGA ACCGTCGAAG GACTATTTCTG CACGACACGA

1741 GTGCAGTAGG AACACATCCT ATTTATTGTG ATGTTGTGGT TTTATTATCT TAAACTCTGT
CACGTCATCC TTGTGTAGGA TAAATAACAC TACAACACCA AAATAATAGA ATTTGAGACA

1801 TCCATACACT TGTATAAATA CATGGATATT TTTATGTACA GAAGTATGTC TCTTAACCAG
AGGTATGTGA ACATATTTAT GTACCTATAA AAATACATGT CTTCATACAG AGAATTGGTC

1861 TTCACTTATT GTACCTGG
AAGTGAATAA CATGGACC

Fig. 1-3



VASCULAR ENDOTHELIAL GROWTH
FACTOR-X
Robert D. Gordon, et al.
Serial No.: 09/468,647

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PREDICTED VEGF-LIKE PROTEIN ENCODED BY INCYTE CONTIG OF 8/12/98

```
1  MNIFLLNLLT  EEVRLYSCTP  RNFSVSIREE  LKRTDTIFWP  GCLLVKRCGG
51 NCACCLHNCN  ECQCVPSKVT  KKYHEVLQLR  PKTGVRGLHK  SLTDVALEHH
101 EECDVCVRGS  TGG
```

Fig. 2



PCR PRIMERS FOR CLONING VEGF-X

vegfx1 AAAATGTATGGATACAACTTAC

vegfx2 GTTTGATGAAAGATTTGGGCTTG

vegfx3 TTTCTAAAGGAAATCAAATTAG

vegfx4 GATAAGATTTGTATCTGATG

vegfx5 GATGTCTCCTCTTTCAG

vegfx6 GCACAACTCCTAATTCTG

vegfx7 AGCACCTGATTCCGTTGC

vegfx8 TAGTACATAGAATGTTCTGG

vegfx9 AAGAGACATACTTCTGTAC

vegfx10 CCAGGTACAATAAGTGAAGTGA

Fig. 3



VARIANTS ISOLATED BY PCR

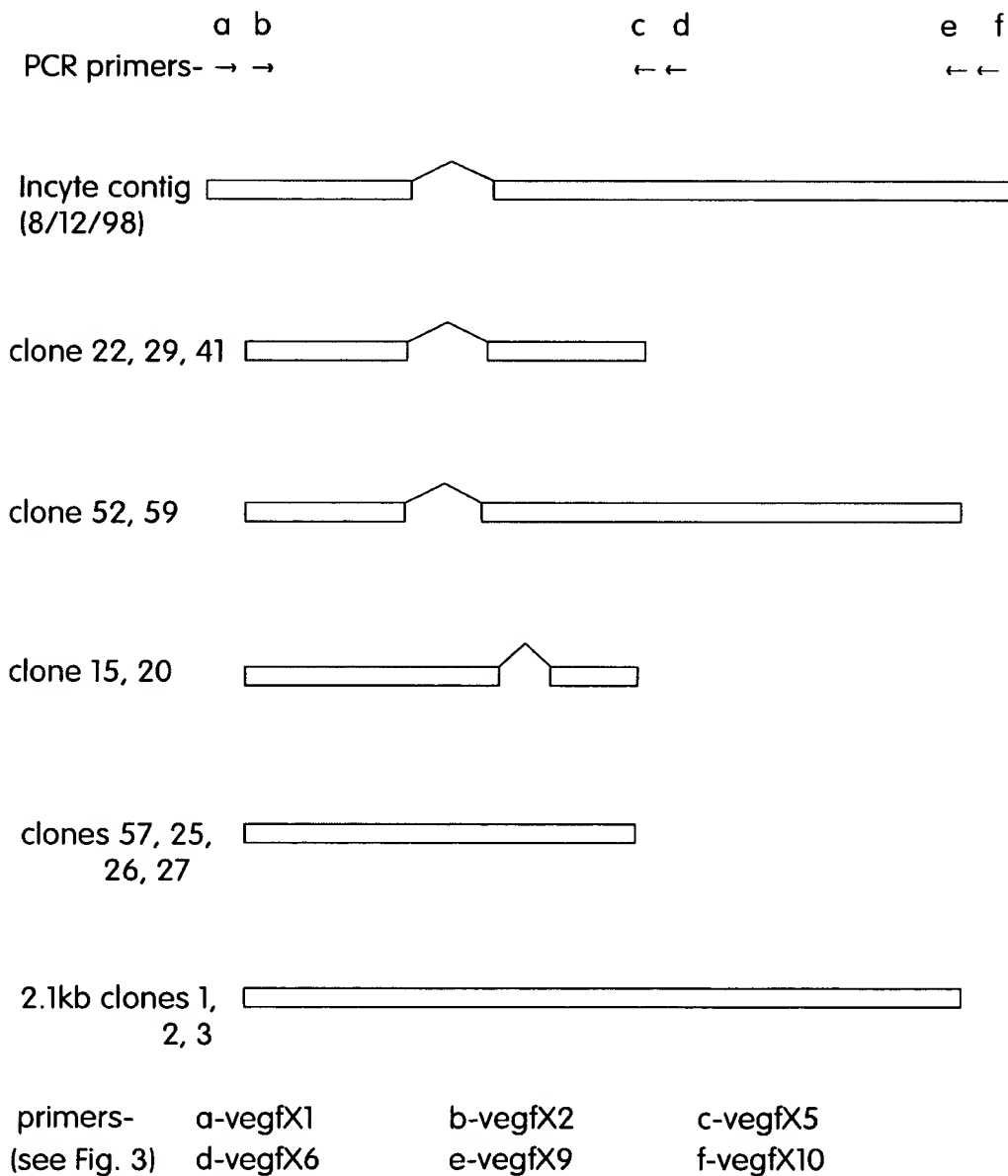


Fig. 4



VASCULAR ENDOTHELIAL GROWTH
FACTOR-X
Robert D. Gordon, et al.
Serial No.: 09/468,647

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VEGF-X 5' RACE PRIMERS

vegfx11 CCTTTAGAAATCTGTTTTCTGGTACAG

vegfx12 GGAAAATATTCATCAGATACAAATCTTATCC

vegfx13 GGTCCAGTGGCAAAGCTGAAGG

vegfx14 CTGGTTCAAGATATCGAATAAGGTCTTCC

Fig. 5



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DNA SEQUENCE ASSEMBLED FROM IN-HOUSE CLONES AND 5'RACE

```
1  TGCCAGAGCA GGTGGGCGCT TCCACCCAG TGCAGCCTTC CCCTGGCGGT GGTGAAAGAG
   ACGGTCTCGT CCACCCGCGA AGGTGGGGTC ACGTCGGAAG GGGACCGCCA CCACTTTCTC

61  ACTCGGGAGT CGCTGCTTCC AAAGTGCCCG CCGTGAGTGA GCTCTCACCC CAGTCAGCCA
   TGAGCCCTCA GCGACGAAGG TTTCACGGGC GGCACCTACT CGAGAGTGGG GTCAGTCGGT

+2  MetSerLeu PheGlyLeuLeu LeuLeuThr SerAlaLeu AlaGlyGlnArg GlnGlyTh
   ]-----

121  AATGAGCCTC TTCGGGCTTC TCCTGCTGAC ATCTGCCCTG GCCGGCCAGA GACAGGGGAC
   TTAATCGGAG AAGCCCGAAG AGGACGACTG TAGACGGGAC CGGCCGGTCT CTGTCCCCTG

+2  rGlnAlaGlu SerAsnLeuSer SerLysPhe GlnPheSer SerAsnLysGlu GlnAsnGl
   -----

181  TCAGGCGGAA TCCAACCTGA GTAGTAAATT CCAGTTTTTC AGCAACAAGG AACAGAACGG
   AGTCCGCCTT AGGTTGGACT CATCATTTAA GGTCAAAAGG TCGTTGTTCC TTGTCTTGCC

+2  yValGlnAsp ProGlnHisGlu ArgIleIle ThrValSer ThrAsnGlySer IleHisSe
   -----

241  AGTACAAGAT CCTCAGCATG AGAGAATTAT TACTGTGTCT ACTAATGGAA GTATTCACAG
   TCATGTTCTA GGAGTCGTAC TCTCTTAATA ATGACACAGA TGATTACCTT CATAAGTGTC

+2  rProArgPhe ProHisThrTyr ProArgAsn ThrValLeu ValTrpArgLeu ValAlaVa
   -----

301  CCCAAGGTTT CCTCATACTT ATCCAAGAAA TACGGTCTTG GTATGGAGAT TAGTAGCAGT
   GGGTTCCAAA GGAGTATGAA TAGGTTCTTT ATGCCAGAAC CATACTCTA ATCATCGTCA

+2  lGluGluAsn ValTrpIleGln LeuThrPhe AspGluArg PheGlyLeuGlu AspProGl
   -----

361  AGAGGAAAAT GTATGGATAC AACTTACGTT TGATGAAAGA TTTGGGCTTG AAGACCCAGA
   TCTCCTTTTA CATACCTATG TTGAATGCAA ACTACTTTCT AAACCCGAAC TTCTGGGTCT

+2  uAspAspIle CysLysTyrAsp PheValGlu ValGluGlu ProSerAspGly ThrIleLe
   -----

421  AGATGACATA TGCAAGTATG ATTTTGTAGA AGTTGAGGAA CCCAGTGATG GAACTATATT
   TCTACTGTAT ACGTTCATAC TAAAACATCT TCAACTCCTT GGGTCACTAC CTTGATATAA

+2  uGlyArgTrp CysGlySerGly ThrValPro GlyLysGln IleSerLysGly AsnGlnIl
   -----

481  AGGGCGCTGG TGTGGTCTG GTACTGTACC AGGAAAACAG ATTTCTAAAG GAAATCAAAT
   TCCCGCGACC ACACCAAGAC CATGACATGG TCCTTTTGTC TAAAGATTTT CTTTAGTTTA

+2  eArgIleArg PheValSerAsp GluTyrPhe ProSerGlu ProGlyPheCys IleHisTy
   -----

541  TAGGATAAGA TTTGTATCTG ATGAATATTT TCCTTCTGAA CCAGGGTTCT GCATCCACTA
   ATCCTATTCT AAACATAGAC TACTTATAAA AGGAAGACTT GGTCCCAAGA CGTAGGTGAT
```

Fig. 6-1



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```
+2 rAsnIleVal MetProGlnPhe ThrGluAla ValSerPro SerValLeuPro ProSerAl
-----
601 CAACATTGTC ATGCCACAAT TCACAGAAGC TGTGAGTCCT TCAGTGCTAC CCCCTTCAGC
    GTTGTAAACAG TACGGTGTTA AGTGTCTTCG AACTCAGGA AGTCACGATG GGGGAAGTCG

+2 aLeuProLeu AspLeuLeuAsn AsnAlaIle ThrAlaPhe SerThrLeuGlu AspLeuIl
-----
661 TTTGCCACTG GACCTGCTTA ATAATGCTAT AACTGCCTTT AGTACCTTGG AAGACCTTAT
    AAACGGTGAC CTGGACGAAT TATTACGATA TTGACGGAAA TCATGGAACC TTCTGGAATA

+2 eArgTyrLeu GluProGluArg TrpGlnLeu AspLeuGlu AspLeuTyrArg ProThrTr
-----
721 TCGATATCTT GAACCAGAGA GATGGCAGTT GGAAGTAGAA GATCTATATA GGCCAACTTG
    AGCTATAGAA CTTGGTCTCT CTACCGTCAA CCTGAATCTT CTAGATATAT CCGGTTGAAC

+2 pGlnLeuLeu GlyLysAlaPhe ValPheGly ArgLysSer ArgValValAsp LeuAsnLe
-----
781 GCAACTTCTT GGCAAGGCTT TTGTTTTTGG AAGAAAATCC AGAGTGGTGG ATCTGAACCT
    CGTTGAAGAA CCGTTCGAA AACAAAAACC TTCTTTTAGG TCTACCACC TAGACTTGGA

+2 uLeuThrGlu GluValArgLeu TyrSerCys ThrProArg AsnPheSerVal SerIleAr
-----
841 TCTAACAGAG GAGGTAAGAT TATACAGCTG CACACCTCGT AACTTCTCAG TGTCCATAAG
    AGATTGTCTC CTCCATTCTA ATATGTCGAC GTGTGGAGCA TTGAAGAGTC ACAGGTATTC

+2 gGluGluLeu LysArgThrAsp ThrIlePhe TrpProGly CysLeuLeuVal LysArgCy
-----
901 GGAAGAACTA AAGAGAACCG ATACCATTTT CTGGCCAGGT TGTCTCCTGG TTAAACGCTG
    CCTTCTTGAT TTCTCTTGGC TATGGTAAAA GACCGGTCCA ACAGAGGACC AATTTGCGAC

+2 sGlyGlyAsn CysAlaCysCys LeuHisAsn CysAsnGlu CysGlnCysVal ProSerLy
-----
961 TGGTGGGAAC TGTGCCTGTT GTCTCCACAA TTGCAATGAA TGTCAATGTG TCCCAAGCAA
    ACCACCCTTG ACACGGACAA CAGAGGTGTT AACGTTACTT ACAGTTACAC AGGGTTCGTT

+2 sValThrLys LysTyrHisGlu ValLeuGln LeuArgPro LysThrGlyVal ArgGlyLe
-----
1021 AGTTACTAAA AAATACCACG AGGTCCTTCA GTTGAGACCA AAGACCGGTG TCAGGGGATT
    TCAATGATTT TTTATGGTGC TCCAGGAAGT CAACTCTGGT TTCTGGCCAC AGTCCCCTAA

+2 uHisLysSer LeuThrAspVal AlaLeuGlu HisHisGlu GluCysAspCys ValCysAr
-----
1081 GCACAAATCA CTCACCGACG TGGCCCTGGA GCACCATGAG GAGTGTGACT GTGTGTGCAG
    CGTGTTTAGT GAGTGGCTGC ACCGGGACCT CGTGGTACTC CTCACACTGA CACACACGTC
```

Fig. 6-2



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+2 gGlySerThr GlyGly
----->

1141	AGGGAGCACA	GGAGGATAGC	CGCATCACCA	CCAGCAGCTC	TTGCCCAGAG	CTGTGCAGTG
	TCCCTCGTGT	CCTCCTATCG	GCGTAGTGGT	GGTCGTCGAG	AACGGGTCTC	GACACGTCAC
1201	CAGTGGCTGA	TTCTATTAGA	GAACGTATGC	GTTATCTCCA	TCCTTAATCT	CAGTTGTTTG
	GTCACCGACT	AAGATAATCT	CTTGCATACG	CAATAGAGGT	AGGAATTAGA	GTCAACAAAC
1261	CTTCAAGGAC	CTTTCATCTT	CAGGATTTAC	AGTGCATTCT	GAAAGAGGAG	ACATCAAACA
	GAAGTTCCTG	GAAAGTAGAA	GTCCTAAATG	TCACGTAAGA	CTTTCTCCTC	TGTAGTTTGT
1321	GAATTAGGAG	TTGTGCAACA	GCTCTTTTGA	GAGGAGGCCT	AAAGGACAGG	AGAAAAGGTC
	CTTAATCCTC	AACACGTTGT	CGAGAAAAC	CTCCTCCGGA	TTTCTGTCC	TCTTTTCCAG
1381	TTCAATCGTG	GAAAGAAAAT	TAAATGTTGT	ATTAAATAGA	TCACCAGCTA	GTTTCAGAGT
	AAGTTAGCAC	CTTTCTTTTA	ATTTACAACA	TAATTTATCT	AGTGGTCGAT	CAAAGTCTCA
1441	TACCATGTAC	GTATTCCACT	AGCTGGGTTT	TGTATTTTCT	TTCTTTTCGAT	ACGGCTTAGG
	ATGGTACATG	CATAAGGTGA	TCGACCCAAG	ACATAAAGTC	AAGAAAGCTA	TGCCGAATCC
1501	GTAATGTCAG	TACAGGAAAA	AAACTGTGCA	AGTGAGCACC	TGATTCCGTT	GCCTTGCTTA
	CATTACAGTC	ATGTCCTTTT	TTTGACACGT	TCACTCGTGG	ACTAAGGCAA	CGGAACGAAT
1561	ACTCTAAAGC	TCCATGTCCT	GGGCCTAAAA	TCGTATAAAA	TCTGGATTTT	TTTTTTTTTT
	TGAGATTTTCG	AGGTACAGGA	CCCGGATTTT	AGCATATTTT	AGACCTAAAA	AAAAAAAAAA
1621	TTTGCTCATA	TTACATATG	TAAACCAGAA	CATTCTATGT	ACTACAAACC	TGGTTTTTAA
	AAACGAGTAT	AAGTGTATAC	ATTTGGTCTT	GTAAGATACA	TGATGTTTGG	ACCAAAAATT
1681	AAAGGAACTA	TGTTGCTATG	AATTAACTT	GTGTCGTGCT	GATAGGACAG	ACTGGATTTT
	TTTCCTTGAT	ACAACGATAC	TTAATTTGAA	CACAGCACGA	CTATCCTGTC	TGACCTAAAA
1741	TCATATTTCT	TATTAAAATT	TCTGCCATTT	AGAAGAAGAG	AACTACATTC	ATGGTTTGGA
	AGTATAAAGA	ATAATTTTAA	AGACGGTAAA	TCTTCTTCTC	TTGATGTAAG	TACCAAACCT
1801	AGAGATAAAC	CTGAAAAGAA	GAGTGGCCTT	ATCTTCACTT	TATCGATAAG	CCAGTTTATT
	TCTCTATTTG	GACTTTTCTT	CTCACCGGAA	TAGAAGTGAA	ATAGCTATTC	GGTCAAATAA
1861	TGTTTCATTG	TGTACATTTT	TATATTCTCC	TTTTGACATT	ATAACTGTTG	GCTTTTCTAA
	ACAAAGTAAC	ACATGTAAAA	ATATAAGAGG	AAAACGTGTA	TATTGACAAC	CGAAAAGATT
1921	TCTTGTTAAA	TATATCTATT	TTTACCAAAG	GTATTTAATA	TTCTTTTTTA	TGACAACTTA
	AGAACAATTT	ATATAGATAA	AAATGGTTTC	CATAAATTAT	AAGAAAAAAT	ACTGTTGAAT

Fig. 6-3



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1981 GATCAACTAT TTTTAGCTTG GTAAATTTTT CTAAACACAA TTGTTATAGC CAGAGGAACA
CTAGTTGATA AAAATCGAAC CATTTAAAAA GATTGTGTGTT AACAAATATCG GTCTCCTTGT

2041 AAGATGATAT AAAATATTGT TGCTCTGACA AAAATACATG TATTTTCATTC TCGTATGGTG
TTCTACTATA TTTTATAACA ACGAGACTGT TTTTATGTAC ATAAAGTAAG AGCATACCAC

2101 CTAGAGTTAG ATTAATCTGC ATTTTAAAAA ACTGAATTGG AATAGAATTG GTAAGTTGCA
GATCTCAATC TAATTAGACG TAAAATTTTT TGACTTAACC TTATCTTAAC CATTCAACGT

2161 AAGACTTTTT GAAAATAATT AAATTATCAT ATCTTCCATT CCTGTTATTG GAGATGAAAA
TTCTGAAAAA CTTTTATTAA TTTAATAGTA TAGAAGGTAA GGACAATAAC CTCTACTTTT

2221 TAAAAAGCAA CTTATGAAAG TAGACATTCA GATCCAGCCA TTAATAACCT ATTCCTTTTT
ATTTTTTCGTT GAATACTTTC ATCTGTAAGT CTAGGTCGGT AATGATTGGA TAAGGAAAAA

2281 TGGGGAAATC TGAGCCTAGC TCAGAAAAAC ATAAAGCACC TTGAAAAAGA CTTGGCAGCT
ACCCCTTTAG ACTCGGATCG AGTCTTTTTG TATTTTCGTGG AACTTTTTTCT GAACCGTCGA

2341 TCCTGATAAA GCGTGCTGTG CTGTGCAGTA GGAACACATC CTATTTATTG TGATGTTGTG
AGGACTATTT CGCACGACAC GACACGTCAT CCTTGTGTAG GATAAATAAC ACTACAACAC

2401 GTTTTATTAT CTTAAACTCT GTTCCATACA CTTGTATAAA TACATGGATA TTTTATGTGTA
CAAAATAATA GAATTTGAGA CAAGGTATGT GAACATATTT ATGTACCTAT AAAAATACAT

2461 CAGAAGTATG TCTCT
GTCTTCATAC AGAGA

Fig. 6-4



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NEW SEQUENCE + INCYTE ESTS

```
1  ATTTGTTTAA ACCTTGGGAA ACTGGTTCAG GTCCAGGTTT TGCTTTGATC CTTTTCAAAA
   TAAACAAATT TGGAACCCTT TGACCAAGTC CAGGTCCAAA ACGAAACTAG GAAAAGTTTT

61  ACTGGAGACA CAGAAGAGGG CTTCTAGGAA AAAGTTTTTG GATGGGATTA TGTGGAAACT
   TGACCTCTGT GTCTTCTCCC GAAGATCCTT TTTCAAAACC CTACCCTAAT ACACCTTTGA

121 ACCCTGCGAT TCTCTGCTGC CAGAGCAGGC TCGGCGCTTC CACCCAGTG CAGCCTTCCC
   TGGGACGCTA AGAGACGACG GTCTCGTCCG AGCCGCGAAG GTGGGGTCAC GTCGGAAGGG

181 CTGGCGGTGG TGAAAGAGAC TCGGGAGTCG CTGCTTCCAA AGTGCCCGCC GTGAGTGAGC
   GACCGCCACC ACTTTCTCTG AGCCCTCAGC GACGAAGGTT TCACGGGCGG CACTCACTCG

+2                               Met SerLeuPhe GlyLeuLeu LeuLeuThrSer AlaLeuAl
   ]-----

241 TCTCACCCCA GTCAGCCAAA TGAGCCTCTT CGGGCTTCTC CTGCTGACAT CTGCCCTGGC
   AGAGTGGGGT CAGTCGGTTT ACTCGGAGAA GCCCGAAGAG GACGACTGTA GACGGGACCG

+2 aGlyGlnArg GlnGlyThrGln AlaGluSer AsnLeuSer SerLysPheGln PheSerSe
   -----

301 CGGCCAGAGA CAGGGGACTC AGGCGGAATC CAACCTGAGT AGTAAATTCC AGTTTTCCAG
   GCCGGTCTCT GTCCCCTGAG TCCGCCTTAG GTTGGACTCA TCATTTAAGG TCAAAGGTC

+2 rAsnLysGlu GlnTyrGlyVal GlnAspPro GlnHisGlu ArgIleIleThr ValSerTh
   -----

361 CAACAAGGAA CAGTACGGAG TACAAGATCC TCAGCATGAG AGAATTATTA CTGTGTCTAC
   GTTGTTCCCTT GTCATGCCTC ATGTTCTAGG AGTCGTACTC TCTTAATAAT GACACAGATG

+2 rAsnGlySer IleHisSerPro ArgPhePro HisThrTyr ProArgAsnThr ValLeuVa
   -----

421 TAATGGAAGT ATTCACAGCC CAAGGTTTCC TCATACTTAT CCAAGAAATA CGGTCTTGGT
   ATTACCTTCA TAAGTGTCGG GTTCCAAAGG AGTATGAATA GGTTCTTTAT GCCAGAACCA

+2 lTrpArgLeu ValAlaValGlu GluAsnVal TrpIleGln LeuThrPheAsp GluArgPh
   -----

481 ATGGAGATTA GTAGCAGTAG AGGAAAATGT ATGGATACAA CTTACGTTTG ATGAAAGATT
   TACCTCTAAT CATCGTCATC TCCTTTTACA TACCTATGTT GAATGCAAAC TACTTTCTAA
```

Fig. 7-1



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```
+2 eGlyLeuGlu AspProGluAsp AspIleCys LysTyrAsp PheValGluVal GluGluPr
-----
541 TGGGCTTGAA GACCCAGAAG ATGACATATG CAAGTATGAT TTTGTAGAAG TTGAGGAACC
    ACCCGAAGCTT CTGGGTCTTC TACTGTATAC GTTCATACTA AAACATCTTC AACTCCTTGG

+2 oSerAspGly ThrIleLeuGly ArgTrpCys GlySerGly ThrValProGly LysGlnIl
-----
601 CAGTGATGGA ACTATATTAG GCGCTGGTG TGGTCTGGT ACTGTACCAG GAAAACAGAT
    GTCCTACCT TGATATAATC CCGCGACCAC ACCAAGACCA TGACATGGTC CTTTGTCTA

+2 eSerLysGly AsnGlnIleArg IleArgPhe ValSerAsp GluTyrPhePro SerGluPr
-----
661 TTCTAAAGGA AATCAAATTA GGATAAGATT TGTATCTGAT GAATATTTTC CTTCTGAACC
    AAGATTTCCT TTAGTTTAAT CCTATTCTAA ACATAGACTA CTTATAAAAG GAAGACTTGG

+2 oGlyPheCys IleHisTyrAsn IleValMet ProGlnPhe ThrGluAlaVal SerProSe
-----
721 AGGGTTCTGC ATCCACTACA ACATTGTCAT GCCACAATTC ACAGAAGCTG TGAGTCCTTC
    TCCCAAGACG TAGGTGATGT TGTAACAGTA CGGTGTAAAG TGTCTTCGAC ACTCAGGAAG

+2 rValLeuPro ProSerAlaLeu ProLeuAsp LeuLeuAsn AsnAlaIleThr AlaPheSe
-----
781 AGTGCTACCC CCTTCAGCTT TGCCACTGGA CTGCTTAAT AATGCTATAA CTGCCTTTAG
    TCACGATGGG GGAAGTCGAA ACGGTGACCT GGACGAATTA TTACGATATT GACGGAAATC

+2 rThrLeuGlu AspLeuIleArg TyrLeuGlu ProGluArg TrpGlnLeuAsp LeuGluAs
-----
841 TACCTTGGA GACCTTATTC GATATCTTGA ACCAGAGAGA TGGCAGTTGG ACTTAGAAGA
    ATGGAACCTT CTGGAATAAG CTATAGAACT TGGTCTCTCT ACCGTCAACC TGAATCTTCT

+2 pLeuTyrArg ProThrTrpGln LeuLeuGly LysAlaPhe ValPheGlyArg LysSerAr
-----
901 TCTATATAGG CCAACTTGGC AACTTCTTGG CAAGGCTTTT GTTTTGGAA GAAAATCCAG
    AGATATATCC GGTGGAACCG TTGAAGAACC GTTCCGAAAA CAAAACCTT CTTTLAGGTC

+2 gValValAsp LeuAsnLeuLeu ThrGluGlu ValArgLeu TyrSerCysThr ProArgAs
-----
961 AGTGGTGGAT CTGAACCTTC TAACAGAGGA GGTAAGATTA TACAGCTGCA CACCTCGTAA
    TCACCACCTA GACTTGGAAG ATTGTCTCCT CCATTCTAAT ATGTCGACGT GTGGAGCATT

+2 nPheSerVal SerIleArgGlu GluLeuLys ArgThrAsp ThrIlePheTrp ProGlyCy
-----
1021 CTTCTCAGTG TCCATAAGGG AAGAACTAAA GAGAACCGAT ACCATTTTCT GGCCAGGTTG
    GAAGAGTCAC AGGTATTCCC TTCTTGATTT CTCTTGGCTA TGGTAAAAGA CCGGTCCAAC
```

Fig. 7-2



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```
+2 sLeuLeuVal LysArgCysGly GlyAsnCys AlaCysCys LeuHisAsnCys AsnGluCy
-----
1081 TCTCCTGGTT AAACGCTGTG GTGGGAACTG TGCCTGTTGT CTCCACAATT GCAATGAATG
AGAGGACCAA TTTGCGACAC CACCCTTGAC ACGGACAACA GAGGTGTTAA CGTTACTTAC

+2 sGlnCysVal ProSerLysVal ThrLysLys TyrHisGlu ValLeuGlnLeu ArgProLy
-----
1141 TCAATGTGTC CCAAGCAAAG TTAATAAAAA ATACCACGAG GTCCTTCAGT TGAGACCAAA
AGTTACACAG GGTTCGTTTC AATGATTTTT TATGGTGCTC CAGGAAGTCA ACTCTGGTTT

+2 sThrGlyVal ArgGlyLeuHis LysSerLeu ThrAspVal AlaLeuGluHis HisGluGl
-----
1201 GACCGGTGTC AGGGGATTGC ACAAATCACT CACCGACGTG GCCCTGGAGC ACCATGAGGA
CTGGCCACAG TCCCCTAACG TGTTTAGTGA GTGGCTGCAC CGGGACCTCG TGGTACTCCT

+2 uCysAspCys ValCysArgGly SerThrGly Gly
----->
1261 GTGTGACTGT GTGTGCAGAG GGAGCACAGG AGGATAGCCG CATCACCACC AGCAGCTCTT
CACACTGACA CACACGTCTC CCTCGTGTCC TCCTATCGGC GTAGTGGTGG TCGTCGAGAA

1321 GCCCAGAGCT GTGCAGTGCA GTGGCTGATT CTATTAGAGA ACGTATGCGT TATCTCCATC
CGGGTCTCGA CACGTCACGT CACCGACTAA GATAATCTCT TGCATACGCA ATAGAGGTAG

1381 CTTAATCTCA GTTGTGTGCT TCAAGGACCT TTCATCTTCA GGATTTACAG TGCATTCTGA
GAATTAGAGT CAACAAACGA AGTTCCTGGA AAGTAGAAGT CCTAAATGTC ACGTAAGACT

1441 AAGAGGAGAC ATCAAACAGA ATTAGGAGTT GTGCAACAGC TCTTTTGAGA GGAGGCCTAA
TTCTCCTCTG TAGTTTGTCT TAATCCTCAA CACGTTGTCT AGAAAACTCT CCTCCGGATT

1501 AGGACAGGAG AAAAGGTCTT CAATCGTGGA AAGAAAATTA AATGTTGTAT TAAATAGATC
TCCTGTCTCT TTTTCCAGAA GTTAGCACCT TTCTTTTAAT TTACAACATA ATTTATCTAG

1561 ACCAGCTAGT TTCAGAGTTA CCATGTACGT ATTCCACTAG CTGGGTTCTG TATTTTCAGTT
TGGTCGATCA AAGTCTCAAT GGTACATGCA TAAGGTGATC GACCCAAGAC ATAAAGTCAA

1621 CTTTCGATAC GGCTTAGGGT AATGTCAGTA CAGGAAAAAA ACTGTGCAAG TGAGCACCTG
GAAAGCTATG CCGAATCCCA TTACAGTCAT GTCCTTTTTT TGACACGTTT ACTCGTGGAC

1681 ATTCCGTTGC CTTGGCTTAA CTCTAAAGCT CCATGTCCTG GGCCTAAAAT CGTATAAAAT
TAAGGCAACG GAACCGAATT GAGATTTCTG GGTACAGGAC CCGGATTTTA GCATATTTTA

1741 CTGGATTTTT TTTTTTTTTT TTGCGCATAT TCACATATGT AAACCAGAAC ATTCTATGTA
GACCTAAAAA AAAAAAAAAA AACGCGTATA AGTGATATCA TTTGGTCTTG TAAGATACAT

1801 CTACAAACCT GGTTTTTTAA AAGGAACAT GTTGCTATGA ATTAACTTG TGTCATGCTG
GATGTTTGA CCAAAAATTT TTCCTTGATA CAACGATACT TAATTTGAAC ACAGTACGAC
```

Fig. 7-3



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1861	ATAGGACAGA	CTGGATTTTT	CATATTTCTT	ATTAAAATTT	CTGCCATTTA	GAAGAAGAGA
	TATCCTGTCT	GACCTAAAAA	GTATAAAGAA	TAATTTTAAA	GACGGTAAAT	CTTCTTCTCT
1921	ACTACATTCA	TGGTTTGGAA	GAGATAAACC	TGAAAAGAAG	AGTGGCCTTA	TCTTCACTTT
	TGATGTAAGT	ACCAAACCTT	CTCTATTTGG	ACTTTTCTTC	TCACCGGAAT	AGAAGTGAAA
1981	ATCGATAAGT	CAGTTTATTT	GTTTCATTGT	GTACATTTTT	ATATTCTCCT	TTTGACATTA
	TAGCTATTCA	GTCAAATAAA	CAAAGTAACA	CATGTAAAAA	TATAAGAGGA	AAACTGTAAT
2041	TAACTGTTGG	CTTTTCTAAT	CTTGTTAAAT	ATATCTATTT	TTACCAAAGG	TATTTAATAT
	ATTGACAACC	GAAAAGATTA	GAACAATTTA	TATAGATAAA	AATGGTTTCC	ATAAATTATA
2101	TCTTTTTTAT	GACAACTTAG	ATCAACTATT	TTTAGCTTGG	TAAATTTTTT	TAAACACAAT
	AGAAAAATA	CTGTTGAATC	TAGTTGATAA	AAATCGAACC	ATTTAAAAAG	ATTTGTGTTA
2161	TGTTATAGCC	AGAGGAACAA	AGATGATATA	AAATATTGTT	GCTCTGACAA	AAATACATGT
	ACAATATCGG	TCTCCTTGTT	TCTACTATAT	TTTATAACAA	CGAGACTGTT	TTTATGTACA
2221	ATTCATTCT	CGTATGGTGC	TAGAGTTAGA	TTAATCTGCA	TTTTAAAAAA	CTGAATTGGA
	TAAAGTAAGA	GCATACCACG	ATCTCAATCT	AATTAGACGT	AAAATTTTTT	GACTTAACCT
2281	ATAGAATTGG	TAAGTTGCAA	AGACTTTTTG	AAAATAATTA	AATTATCATA	TCTTCCATTC
	TATCTTAACC	ATTCAACGTT	TCTGAAAAAC	TTTTATTAAT	TTAATAGTAT	AGAAGGTAAG
2341	CTGTTATTGG	AGATGAAAAAT	AAAAAGCAAC	TTATGAAAAGT	AGACATTGAG	ATCCAGCCAT
	GACAATAACC	TCTACTTTTA	TTTTTCGTTG	AATACTTTCA	TCTGTAAGTC	TAGGTCGGTA
2401	TACTAACCTA	TTCCTTTTTT	GGGGAAATCT	GAGCCTAGCT	CAGAAAAACA	TAAAGCACCT
	ATGATTGGAT	AAGGAAAAAA	CCCCTTTAGA	CTCGGATCGA	GTCTTTTTGT	ATTTTCGTGA
2461	TGAAAAAGAC	TTGGCAGCTT	CCTGATAAAG	CGTGCTGTGC	TGTGCAGTAG	GAACACATCC
	ACTTTTTCTG	AACCGTCGAA	GGACTATTTT	GCACGACACG	ACACGTCATC	CTTGTGTAGG
2521	TATTTATTGT	GATGTTGTGG	TTTTATTATC	TTAAACTCTG	TTCCATACAC	TTGTATAAAT
	ATAAATAACA	CTACAACACC	AAAATAATAG	AATTTGAGAC	AAGGTATGTG	AACATATTTA
2581	ACATGGATAT	TTTTATGTAC	AGAAGTATGT	CTCTTAACCA	GTTCACTTAT	TGTACTCTGG
	TGTACCTATA	AAAATACATG	TCTTCATACA	GAGAATTGGT	CAAGTGAATA	ACATGAGACC
2641	CAATTTAAAA	GAAAATCAGT	AAAATATTTT	GCTTGTAATA	TGCTTAATAT	CGTGCCTAGG
	GTTAAATTTT	CTTTTAGTCA	TTTTATAAAA	CGAACATTTT	ACGAATTATA	GCACGGATCC
2701	TTATGTGGTG	ACTATTTGAA	TCAAAAATGT	ATTGAATCAT	CAAATAAAAG	AATGTGGCTA
	AATACACCAC	TGATAAACTT	AGTTTTTACA	TAACCTAGTA	GTTTATTTTC	TTACACCGAT
2761	TTTTGGGGAG	AAAATT				
	AAAACCCCTC	TTTTAA				

Fig. 7-4



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ADDITIONAL OLIGONUCLEOTIDES USED FOR AMPLIFICATION
OF ENTIRE CODING REGION

5' -1 TTTGTTTAAACCTTGGGAAACTGG

5' -2 GTCCAGGTTTTGCTTTGATCC

Fig. 8



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DNA SEQUENCE OF CLONES 4 & 7, IDENTICAL CLONES CONTAINING THE
ENTIRE OPEN READING FRAME

```
1  TTTGTTTAAA CCTTGGGAAA CTGGTTCAGG TCCAGGTTTT GCTTTGATCC TTTTCAAAAA
   AAACAAATTT GGAACCCTTT GACCAAGTCC AGGTCCAAAA CGAAACTAGG AAAAGTTTTT

61  CTGGAGACAC AGAAGAGGGC TCTAGGAAAA AGTTTTGGAT GGGATTATGT GGAAACTACC
   GACCTCTGTG TCTTCTCCCG AGATCCTTTT TCAAAACCTA CCCTAATACA CTTTGTATGG

121 CTGCGATTCT CTGCTGCCAG AGCAGGCTCG GCGCTTCCAC CCCAGTGCAG CTTTCCCCTG
   GACGCTAAGA GACGACGGTC TCGTCCGAGC CGCGAAGGTG GGGTCACGTC GGAAGGGGAC

181 GCGGTGGTGA AAGAGACTCG GGAGTCGCTG CTTCCAAAGT GCCCGCCGTG AGTGAGCTCT
   CGCCACCACT TTCTCTGAGC CCTCAGCGAC GAAGGTTTCA CGGGCGGCAC TCACTCGAGA

+2                               MetSer LeuPheGly LeuLeuLeu LeuThrSerAla LeuAlaGl
   ]-----

241 CACCCAGTC AGCCAAATGA GCCTCTTCGG GCTTCTCCTG CTGACATCTG CCCTGGCCGG
   GTGGGGTCAG TCGGTTTACT CGGAGAAAGCC CGAAGAGGAC GACTGTAGAC GGGACCGGCC

+2 yGlnArgGln GlyThrGlnAla GluSerAsn LeuSerSer LysPheGlnPhe SerSerAs
   -----

301 CCAGAGACAG GGGACTCAGG CGGAATCCAA CCTGAGTAGT AAATTCCAGT TTTCCAGCAA
   GGTCTCTGTC CCCTGAGTCC GCCTTAGGTT GGACTCATCA TTTAAGGTCA AAAGGTCGTT

+2 nLysGluGln AsnGlyValGln AspProGln HisGluArg IleIleThrVal SerThrAs
   -----

361 CAAGGAACAG AACGGAGTAC AAGATCCTCA GCATGAGAGA ATTATTACTG TGTCTACTAA
   GTTCCTTGTC TTGCCTCATG TTCTAGGAGT CGTACTCTCT TAATAATGAC ACAGATGATT

+2 nGlySerIle HisSerProArg PheProHis ThrTyrPro ArgAsnThrVal LeuValTr
   -----

421 TGGAAGTATT CACAGCCCAA GGTTTCCTCA TACTTATCCA AGAAATACGG TCTTGGTATG
   ACCTTCATAA GTGTCGGGTT CCAAAGGAGT ATGAATAGGT TCTTTATGCC AGAACCATAC

+2 pArgLeuVal AlaValGluGlu AsnValTrp IleGlnLeu ThrPheAspGlu ArgPheGl
   -----

481 GAGATTAGTA GCAGTAGAGG AAAATGTATG GATACAACTT ACGTTTGATG AAAGATTTGG
   CTCTAATCAT CGTCATCTCC TTTTACATAC CTATGTTGAA TGCAAACCTAC TTTCTAAACC

+2 yLeuGluAsp ProGluAspAsp IleCysLys TyrAspPhe ValGluValGlu GluProSe
   -----

541 GCTTGAAGAC CCAGAAGATG ACATATGCAA GTATGATTTT GTAGAAGTTG AGGAACCCAG
   CGAACTTCTG GGTCTTCTAC TGTATACGTT CATACTAAAA CATCTTCAAC TCCTTGGGTC
```

Fig. 9-1



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```
+2 rAspGlyThr IleLeuGlyArg TrpCysGly SerGlyThr ValProGlyLys GlnIleSe
-----
601 TGATGGAAC TATATTAGGGC GCTGGTGTGG TTCTGGTACT GTACCAGGAA AACAGATTTCT
ACTACCTTGA TATAATCCCG CGACCACACC AAGACCATGA CATGGTCCTT TTGTCTAAAG

+2 rLysGlyAsn GlnIleArgIle ArgPheVal SerAspGlu TyrPheProSer GluProGlu
-----
661 TAAAGGAAAT CAAATTAGGA TAAGATTTGT ATCTGATGAA TATTTTCCTT CTGAACCAGG
ATTTCTTTTA GTTTAATCCT ATTCTAAACA TAGACTACTT ATAAAAGGAA GACTTGGTCC

+2 yPheCysIle HisTyrAsnIle ValMetPro GlnPheThr GluAlaValSer ProSerVal
-----
721 GTTCTGCATC CACTACAACA TTGTCATGCC ACAATTCACA GAAGCTGTGA GTCCTTCAGT
CAAGACGTAG GTGATGTTGT AACAGTACGG TGTTAAGTGT CTTTCGACACT CAGGAAGTCA

+2 lLeuProPro SerAlaLeuPro LeuAspLeu LeuAsnAsn AlaIleThrAla PheSerThr
-----
781 GCTACCCCTC TCAGCTTTGC CACTGGACCT GCTTAATAAT GCTATAACTG CCTTTAGTAC
CGATGGGGGA AGTCGAAACG GTGACCTGGA CGAATTATTA CGATATTGAC GGAAATCATG

+2 rLeuGluAsp LeuIleArgTyr LeuGluPro GluArgTrp GlnLeuAspLeu GluAspLeu
-----
841 CTTGGAAGAC CTTATTTCGAT ATCTTGAACC AGAGAGATGG CAGTTGGACT TAGAAGATCT
GAACCTTCTG GAATAAGCTA TAGAACTTGG TCTCTCTACC GTCAACCTGA ATCTTCTAGA

+2 uTyrArgPro ThrTrpGlnLeu LeuGlyLys AlaPheVal PheGlyArgLys SerArgVal
-----
901 ATATAGGCCA ACTTGGCAAC TTCTTGGCAA GGCTTTTGTT TTTGGAAGAA AATCCAGAGT
TATATCCGGT TGAACCGTTG AAGAACCGTT CCGAAAACAA AAACCTTCTT TTAGGTCTCA

+2 lValAspLeu AsnLeuLeuThr GluGluVal ArgLeuTyr SerCysThrPro ArgAsnPhe
-----
961 GGTGGATCTG AACCTTCTAA CAGAGGAGGT AAGATTATAC AGCTGCACAC CTCGTAACCT
CCACCTAGAC TTGGAAGATT GTCTCCTCCA TTCTAATATG TCGACGTGTG GAGCATTGAA

+2 eSerValSer IleArgGluGlu LeuLysArg ThrAspThr IlePheTrpPro GlyCysLeu
-----
1021 CTCAGTGTCC ATAAGGGAAG AACTAAAGAG AACCGATACC ATTTTCTGGC CAGGTTGTCT
GAGTCACAGG TATTCCCTTC TTGATTCTC TTGGCTATGG TAAAAGACCG GTCCAACAGA

+2 uLeuValLys ArgCysGlyGly AsnCysAla CysCysLeu HisAsnCysAsn GluCysGlu
-----
1081 CCTGGTTAAA CGCTGTGGTG GGAAGTGTGC CTGTTGTCTC CACAATTGCA ATGAATGTCA
GGACCAATTT GCGACACCAC CCTTGACACG GACAACAGAG GTGTTAACGT TACTTACAGT
```

Fig. 9-2



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```
+2 nCysValPro SerLysValThr LysLysTyr HisGluVal LeuGlnLeuArg ProLysTh
-----
1141 ATGTGTCCCA AGCAAAGTTA CTAAAAAATA CCACGAGGTC CTTCA GTTGA GACCAAAGAC
    TACACAGGGT TCGTTTCAAT GATTTTTTAT GGTGCTCCAG GAAGTCAACT CTGGTTTCTG

+2 rGlyValArg GlyLeuHisLys SerLeuThr AspValAla LeuGluHisHis GluGluCy
-----
1201 CGGTGTCAGG GGATTGCACA AATCACTCAC CGACGTGGCC CTGGAGCACC ATGAGGAGTG
    GCCACAGTCC CCTAACGTGT TTAGTGAGTG GCTGCACCGG GACCTCGTGG TACTCCTCAC

+2 sAspCysVal CysArgGlySer ThrGlyGly
----->
1261 TGA CTGTGTG TGCAGAGGGA GCACAGGAGG ATAGCCGCAT CACCACCAGC AGCTCTTGCC
    ACTGACACAC ACGTCTCCCT CGTGTCTCTCC TATCGGCGTA GTGGTGGTCG TCGAGAACGG

1321 CAGAGCTGTG CAGTGCAGTG GCTGATTCTA TTAGAGAACG TATGCGTTAT CTCCATCCTT
    GTCTCGACAC GTCACGTCAC CGACTAAGAT AATCTCTTGC ATACGCAATA GAGGTAGGAA

1381 AATCTCAGTT GTTTGCTTCA AGGACCTTTC ATCTTCAGGA TTTACAGTGC ATTCTGAAAG
    TTAGAGTCAA CAAACGAAGT TCCTGGAAAG TAGAAGTCCT AAATGTCACG TAAGACTTTC

1441 AGGAGACATC AAACAGAATT AGGAGTTGTG CAA
    TCCTCTGTAG TTTGTCTTAA TCCTCAACAC GTT
```

Fig. 9-3



VASCULAR ENDOTHELIAL GROWTH
FACTOR-X
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PREDICTED FULL-LENGTH POLYPEPTIDE SEQUENCE

1 MSLFGLLLLT SALAGQRQGT QAESNLSSKF QFSSNKEQYG VQDPQHERII
51 TVSTNGSIHS PRFPHTYPRN TVLVWRLVAV EENVWIQLTF DERFGLEDPE
101 DDICKYDFVE VEEPSDGTIL GRWCGSGTVP GKQISKGNQI RIRFVSDEYF
151 PSEPGFCIHY NIVMPQFTEA VSPSVLPSPA LPLDLLNNAI TAFSTLEDLI
201 RYLEPERWQL DLEDLYRPTW QLLGKAFVFG RKSRVVDLNL LTEEVRLYSC
251 TPRNFSVSIR EELKRTDTIF WPGCLLVKRC GGNCACCLHN CNECQCVPSK
301 VTKKYHEVLQ LRPKTGVRGL HKSLTDVALE HHEECDVCR GSTGG

Fig. 10



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ALIGNMENT OF VEGF-X WITH OTHER VEGFs

```

                                *      20      *      40      *
VEGF_HUMAN : ----- : -
PLGF_HUMAN : ----- : -
VEGB_HUMAN : ----- : -
VEGC_HUMAN : ----- : -
VEGD_HUMAN : ----- : -
990126vegx : MSLFGLLLTSALAGQRQGTQAESNLSSKFQFSSNKEQNGVQDPQHERII : 50

                                60      *      80      *      100
VEGF_HUMAN : ----- : -
PLGF_HUMAN : ----- : -
VEGB_HUMAN : ----- : -
VEGC_HUMAN : ----- : -
VEGD_HUMAN : ----- : -
990126vegx : TVSTNGSIHSPRFPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPE : 100

                                *      120      *      140      *
VEGF_HUMAN : ----- : -
PLGF_HUMAN : ----- : -
VEGB_HUMAN : ----- : -
VEGC_HUMAN : -----MHLLGFFSVACSLLAALLPGPREAPAAAA : 30
VEGD_HUMAN : -----MYREWVVNV : 10
990126vegx : DDICKYDFVEV--EEPSDGTILGRWCGSGTVPQKQISKGNQIRIRFVSDE : 148

                                160      *      180      *      200
VEGF_HUMAN : -----MN : 2
PLGF_HUMAN : -----MP : 2
VEGB_HUMAN : ----- : -
VEGC_HUMAN : AFESGLDLSDAEPDAGEATAYASKDLEEQLRSVSSVDELMTVLYPEYWKM : 80
VEGD_HUMAN : FMMLYVQLVQGSSNEHGPVKRSSQSTLERSEQQIRAASSLEELLRITHSE : 60
990126vegx : YFPSEPGFCIHYNIVMPQFTEAVSPSVLPSPALPLDLLNNAITAFSTLED : 198

                                *      220      *      240      *
VEGF_HUMAN : FLLSWVHWSLALLLYLHHAWSQAAPMAEGGGQNHHEVVKFMD-VYORSY : 51
PLGF_HUMAN : VMRLFPCFLQLLAGLALPAVPPQWALSAGNGSSEVEVVPFQE-VWGRSY : 51
VEGB_HUMAN : ---MSPLLRRLLLAALLQLAPAQAPVSQPDAPGHQRKVVSVID-VYTRAT : 46
VEGC_HUMAN : YKQLRKGGWQHNRQANLNSRTEETIKFAAAHYNTIELKSIDNEWRTQ : 130
VEGD_HUMAN : DWKLWRCRLRLKSFTSMDSRSASHRSTRFAATFYDIETLKVIDEEWRTQ : 110
990126vegx : LIRYLEPERWQLLEDLYRPTWQLLGKAFVFGKSRVVDLNLTEEVRLY : 248
```

Fig. 11-1



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```
                260          *          280          *          300
VEGF_HUMAN : CHPIETLVDIFQEYPDEIEYIFKPSCVPLMRCG---CCND--EGLECV : 96
PLGF_HUMAN : CRALERLVDVVSSEYPSEVEHMFSPSCVSLLRCTG---CCGD--ENLHCVP : 96
VEGB_HUMAN : CQPREVVVPLTVELMGTVAKQLVPSCVTVQRCG---CCPD--DGLECV : 91
VEGC_HUMAN : CMPREVCIDVGKEFGVATNTFFKPPCVSVYRCG---CONS--EGLQCMN : 175
VEGD_HUMAN : CSPRETCVEVASSELGKSTNTFFKPPCVNVFRCG---CONE--ESLICMN : 155
990126vegx : SCTPRNFSVSIREELKRTDTIEFWGCLLVKRCGNCACCLHNCNECQCV : 298
```

```
                *          320          *          340          *
VEGF_HUMAN : TEESNTTMOILMRKPHQG-----QHIGEMSFLQHNKCECRPKKDRARQEK : 141
PLGF_HUMAN : VETANVTMOILKIRSGDR-----PSYVELTFSQHVRCECRPLREKMKPER : 141
VEGB_HUMAN : TGQHQRMOILMIRYPS-----SOLGEMSLEEHSQCECRPKKKDSAVKP : 135
VEGC_HUMAN : TSTSLSKTLFEITVPLSQG---PKPVTISFANHTSCROMSKLDVYRQVH : 222
VEGD_HUMAN : TSTSLSKQLFEISVPLTSV---PELVPKVANHTGCKCLFTAPRHPYSI : 202
990126vegx : SKVTKKYHEVLQLRPKTGVRGLHKS LTDVALEHHEECDVCVRGSTGG--- : 345
```

```
                360          *          380          *          400
VEGF_HUMAN : KSVRGKGKGQKRKRKKSRYKSWSP----- : 166
PLGF_HUMAN : ----- : -
VEGB_HUMAN : DSPR----- : 139
VEGC_HUMAN : SIIRSLPATLPQCAANKTCPTNYMWNHICRLAQEDFMFSSDAGDDS : 272
VEGD_HUMAN : IRRSIQIPEEDRCSHKKLCPIDMLWDSNKCKCVLQENPLAGT----- : 246
990126vegx : ----- : -
```

```
                *          420          *          440          *
VEGF_HUMAN : ----- : -
PLGF_HUMAN : ----- : -
VEGB_HUMAN : ----- : -
VEGC_HUMAN : TDGFHDICGPNKELDEETCQCVCRAGLRPASCGPHKELDRNSCQCVCKNK : 322
VEGD_HUMAN : -----EDHSHLQEPALCGP : 260
990126vegx : ----- : -
```

```
                460          *          480          *          500
VEGF_HUMAN : -----CGPCSERRKHLFVQDPQTCKC-SCKNTDSRCKARQLELNER : 206
PLGF_HUMAN : -----CGDAVPRR----- : 149
VEGB_HUMAN : -----PLCPRCTQHHQRPDPRTCRRCRRRSFLRCQGRGLELNP : 179
VEGC_HUMAN : LFPSQCGANREFDENTCQCVCKRTCPRNQPLNPGKACECTESPQKCLLK : 372
VEGD_HUMAN : HMMFDEDRCECVCKTPCPKDLIQHPKNCSCFECKESLETCCQKHKLPHPD : 310
990126vegx : ----- : -
```

Fig. 11-2



VASCULAR ENDOTHELIAL GROWTH
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	*	520	*	540	*	
VEGF_HUMAN	:	TCRCDKPRR-----	:	215		
PLGF_HUMAN	:	-----	:	-		
VEGB_HUMAN	:	TCRCRKLRR-----	:	188		
VEGC_HUMAN	:	GKKFHHQTCSCYRRPCTNRQKACEPGFSYSEEVCRCVPSYWKRPQMS---	:	419		
VEGD_HUMAN	:	TCSCEDRCPFHTRPCASGKTACAKHCRFPKEKRAAQGPHSRKNP-----	:	354		
990126vegx	:	-----	:	-		

Fig. 11-3



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VARIANT POLYPEPTIDE SEQUENCES

	*	20	*	40	*	
FL_seq	:	MSLFGLLLTSALAGQRQGTQAESNLSSKFQFSSNKEQNGVQDPQHERII				: 50
clone41	:	MSLFGLLLTSALAGQRQGTQAESNLSSKFQFSSNKEQNGVQDPQHERII				: 50
clone20	:	MSLFGLLLTSALAGQRQGTQAESNLSSKFQFSSNKEQNGVQDPQHERII				: 50
		60	*	80	*	100
FL_seq	:	TVSTNGSIHSPRFPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPE				: 100
clone41	:	TVSTNGSIHSPRFPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPE				: 100
clone20	:	TVSTNGSIHSPRFPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPE				: 100
		*	120	*	140	*
FL_seq	:	DDICKYDFVEVEEPSDGTILGRWCGSGTVPKGQISKGNQIRIRFVSDEYF				: 150
clone41	:	DDICKYDFVEVEEPSDGTILGRWCGSGTVPKGQISKGNQIRIRFVSDEYF				: 150
clone20	:	DDICKYDFVEVEEPSDGTILGRWCGSGTVPKGQISKGNQIRIRFVSDEYF				: 150
		160	*	180	*	200
FL_seq	:	PSEPGFCIHYNIIVMPQFTEAVSPSVLPPSALPLDLLNNAITAFSTLEDLI				: 200
clone41	:	PSEPSNRGGKIIQLHTS-----				: 167
clone20	:	PSEPGFCIHYNIIVMPQFTEAVSPSVLPPSALPLDLLNNAITAFSTLEDLI				: 200
		*	220	*	240	*
FL_seq	:	RYLEPERWQLDLEDLYRPTWQLLGKAFVFGKSRVVDLNLLE				: 250
clone41	:	-----				: -
clone20	:	RYLEPERWQLDLEDLYRPTWQLLGKAFVFGKSRVVDLNLLE				: 243
		260	*	280	*	300
FL_seq	:	TPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPSK				: 300
clone41	:	-----				: -
clone20	:	-----				: -
		*	320	*	340	
FL_seq	:	VTKKYHEVLQLRPKTGVRGLHKS LTDVALEHHEECDCVCRGSTGG				: 345
clone41	:	-----				: -
clone20	:	-----EVLQLRPKTGVRGLHKS LTDVALEHHEECDCVCRGSTGG				: 282

Fig. 12



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PRIMERS FOR EXPRESSION OF VEGF-X

E. coli EXPRESSION OF DOMAIN-

vegx-6 AATTGGATCCGAGAGTGGTGGATCTGAACC

vegx-7 AATTGGATCCGGAAGAAAATCCAGAGTGG

vegx-8 GGTGAATTCATTATTTTTTAGTAACTTTGCTTGGGACAC

vegx-9 AATTGAATTCATTATCCTCCTGTGCTCCCTC

BACULOVIRUS/INSECT CELL EXPRESSION OF FULL-LENGTH PROTEIN-

vegbac1

AATTGGATCCGGAGTCTCACCATCACCACCATCATGAATCCAACCTGAGTAGTAAATTCC

vegbac2

AATTGAATTCGCTATCCTCCTGTGCTCCCTCTGC

Fig. 13



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1 >3993180H1  LUNGNON03  INCYTE
2 CACAAATCACTCACCGACGTGGCCCTGGAGCACCATGAGGNGTGTGACTGTGTGTGCAGAGG
3 GAGCACAGGAGGATAGCCGCATCACCACCAGCAGCTCTTGCCCAGAGCTGTGCAGTGCAGTG
4 GCTGATTCTATTAGAGAACGTATGCGTTATCTCCATCCTTAATCTCAGTTGTTTGCTTCAAG
5 GACCTTTTCATCTTCAGGATTTACAGTGCATTCTGAAAGAGGAGACATCAAACAGAATTAGGA
6 GTTGTGCAACAGCTCTTTTGAGAGGAGGCTAAAGGACAGGAGAAANAGGTCTT
7 >3510192H1  CONCNOT01  INCYTE
8 TGCAGTGCAGTGGCTGATTCTATTAGAGAACGTATGCGTTATCTCCATCCTTAATCTCAGTT
9 GTTTGCTTCAAGGACCTTTTCATCTTCAGGATTTACAGTGCATTCTGAAAGAGGAGACATCAA
10 ACAGAATTAGGAGTTGTGCAACAGCTCTTTTGAGAGGAGGCCTAAAGGACAGGAGAAAAGGT
11 CTTCAATCGTGGAAAGAAAATTAAATGTTGTATTAAATAGATCACCAGCTAGTTTCAGAGTT
12 ACCATGTACGTATTCCACTAGCTGGGTTCTGTATTT
13 >2559870H1  ADRETUT01  INCYTE
14 CACGAGGTCCTTCAGTTGAGACCAAAGACCGGTGTCAGGGGATTGCACAAATCACTCACCGA
15 CGTGGCCCTGGAGCACCATGAGGAGTGTGACTGTGTGTGCAGAGGGAGCACAGGGGGATAGC
16 CGCATCACCACCAGCAGCTCTTGCCCAGAGCTGTGCAGTGCAGTGGCTGATTCTATTAGAGA
17 ACGTATGCGTTATCTCCATCCTTAATCTCAGTTGTTTGCTTCAAGGACCTTTTCATCTTCAGG
18 ATTTACAGTGCATTCTGAAAGAGGAGA
19 >3979767H1  LUNGTUT08  INCYTE
20 GGAGGATAGCCGCATCACCACCAGCAGCTCTTGCCCAGAGCTGTGCAGTGCAGTGGCTGATT
21 CTATTAGAGAACGTATGCGTTATCTCCATCCTTAATCTCAGTTGTTTGCTTCAAGGACCTTT
22 CATCTTCAGGATTTACAGTGCATTCTGAAAGAGGAGACATCAAACAGAATTAGGAGTTGTGC
23 AACAGCTCTTTTGAGAGGAGGCCTAAAGGACAGGAGAAAAGGTCTTCAATCGTGGAAAGAAAN
24 ATTAAATGTTGTATTAAATAGACACCAGCT
25 >3980011H1  LUNGTUT08  INCYTE
26 GGAGGATAGCCGCATCACCACCAGCAGCTCTTGCCCAGAGCTGTGCAGTGCAGTGGCTGATT
27 CTATTAGAGAACGTATGCGTTATCTCCATCCTTAATCTCAGTTGTTTGCTTCAAGGACCTTT
28 CATCTTCAGGATTTACATGCATTCTGAAAGAGGAGACATCAAACAGAATTAGGAGTTGTGCA
29 ACAGCTCTTTTGAGAGGAGGCCTAAAGGACAGGAGAAAAGGTCTTCAATCGTGGAAAGAAAA
30 TTAAATGTTGTATTAAATAGATCACCA
31 >4825396H1  BLADDIT01  INCYTE
32 GAGAACC GATACCATTTTCTGGCCAGGTTGTCTCCTGGTTAAACGCTGTGGTGGGAACTGTG
33 CCTGTTGTCTCCACAATTGCAATGAATGTCAATGTGTCCCAAGCAAAGTTACTAAAAAATAC
34 CACGAGGTCCTTCAGTTGAGACCAAAGACCGGTGTCAGGGGATTGCACAAATCACTCACCGA
35 CGTGGCCCTGGAGCACCATGAGGAGTGTGACTGTGTGTGCAGAGGGAGCACAGGAGGATAGC
36 CGCATCACCACCA
37 >3073703H1  BONEUNT01  INCYTE
38 AGAAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGGAGGTAAGATTATACAGCTGCAC
39 ACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATACCATTTTCTGGC
40 CAGGTTGTCTCCTGGTTAAACGCTGTGGTGGGAACTGTGCCTGTTGTCTCCACAATTGCAAT
41 GAATGTCAATGTGTCCCAAGCAAAGTTACTAAAAAATACCACGAGGTCCTTCAGTTGAGACC
42 AAAGACCGGTGTCAGGGGATTGCACAAATCA
```

Fig. 14-1



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43 >1302516H1 PLACNOT02 INCYTE
44 AGGAAATCAAATTAGGATAAGATTTGTATCTGATGAATATTTTCCTTCTGAACCTTCTAACA
45 GAGGAGGTAAGATTATACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACT
46 AAAGAGAACCGATAACCATTTTCTGGCCAGGTTGTCTCCTGGTTAAACGCTGTGGTGGGAACT
47 GTGCCTGTTGTCTCCACAATTGCAATGAATGTCAATGTGTCCCAAGCAAAGTTACTAAAAA
48 ATACCACGAGGTCC
49 >3684109H1 HEANOT01 INCYTE
50 ATTTTCATCTTCAGGATTTACAGTGCATTCTGAAANAGGAGAAATCAAACANAATTAGGAGTT
51 GTGCAACAGCTCTTTTGAGAGGAGGCCTAAAGGACAGGAGAAAAGGTCTTCAATCGTGGAAA
52 NAAAATTAAATGTTGTATTAAATAGATCACCAGCTAGTTTCAGAGTTACCATGTACGTATTC
53 CACTAGCTGGGTTCTGTATTTTCAGTTCTTTTCGATACGGCTTAGGGTAATGTCAGTACAGGAA
54 AAAAAGTGTGCAAGTGAGCACCTGATTCCGTTGCCTTGCTT
55 >4713188H1 BRAIHCT01 INCYTE
56 CAAAGTTACTAAAAAATACCACGAGGTCCTTCAGTTGAGACCAAAGACCGGTGTCAGGGGAT
57 TGCACAAATCACTACCGACGTGGCCCTGGAGCACCATGAGGAGTGTGACTGTGTGTGCAGA
58 GGGAGCACAGGAGGATAGCCGCATCACCACCAGCAGCTCTTGCCAGAGCTGTGCAGTGCAG
59 TGGCTGATTCTATTAGAGAACGTATGCGTTATCTCCATCCTTAATCTCAGTTGTTTGCT
60 >458823H1 KERANOT01 INCYTE
61 ANGAGTTGCCAGAGCTGTGCAGTGCAGTGGCTGATTCTATTAGAGAACGTATGCGTTATCT
62 CCATCCTTAATCTCAGTTGTTTGNTTCAAGGACCTTTTCATCTTCAGGATTTACAGTGCATTCT
63 TGAAAGAGGAGACATCAAACAGAATTAGGAGTTGTGCAACAGCTCTTTTGAGAGGAGGCCTA
64 AAGGNCAGGAGAAAAGGTCTTCAATCGTGGAAAGAAAATTAAATGTTGTATTAAATAGATC
65 >1303909H1 PLACNOT02 INCYTE
66 AGGAAATCAAATTAGGATAAGATTTGTATCTGATGAATATTTTCCTTCTGAACCTTCTAACA
67 GAGGAGGTAAGATTATACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACT
68 AAAGAGAACCGATAACCATTTTCTGGCCAGGTTGTCTCCTGGTTAAACGCTGTGGTGGGAACT
69 GTGCCTGTTGTCTCCACAATTGCAATGAATGTCAATGTGTCCCAAG
70 >2739211H1 OVARNOT09 INCYTE
71 GTGCATTCTGAAAGAGGAGACATCAAACAGAATTAGGAGTTGTGCAACAGCTCTTTTGAGAG
72 GAGGCCTAAAGGACAGGAGAAAAGGTCTTCAATCGTGGAAGAAAATTAAATGTTGTATTAA
73 ATAGATCACCAGCTAGTTTCAGAGTTACCATGTACGTATTCCACTAGCTGGGTTCTGTATTT
74 CAGTTCTTTTCGATACGGCTTAGGGTAATGTCAGTACAGGAAAAAACTGTGCAAGTGAGCAC
75 CTGAT
76 >3325591H1 PTHYNOT03 INCYTE
77 TGCAACAGCTCTTTTGAGAGGAGGCCTAAAGGACAGGAGAAAAGGTCTTCAATCGTGGAAG
78 AAAATTAAATGTTGTATTAAATAGATCACCAGCTAGTTTCAGAGTTACCATGTACGTATTCC
79 ACTAGCTGGGTTCTGTATTTTCAGTTCTTTTCGATACGGCTTAGGGTAATGTCAGTACAGGAAA
80 AAACTGTGCAAGTGAGCACCTGATTCCGTTGCCTTGCTTAACCCTAAAGCNCCATGTCNNG
81 GGCNAAAANCGAAAAAT

Fig. 14-2



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82 >3733565H1 SMCCNOS01 INCYTE
83 CCTTAATCTCAGTTGTTTGCTTCAAGGACCTTTCATCTTCAGGATTTACAGTGCATTCTGNA
84 AGANGAGACATCAAACAGAATTAGGNGTTGTGCAAAAGCTCTTTTGAGAGGAGGCCTAAAGG
85 ACAGGAGAAAAGGTCTNCAATCGTGGAAAGNAAATTAAATGTTGTATNAAATNGATCACCAG
86 CTAGTTTCAGAGTTACCATGTACGTATTCCACTAGCTGGGNCNGTATTCAGTCTTTCGGAAC
87 GGCTTAGGGTAATGTCAGTACAGGANAAAACTGTGCAGTGAG
88 >3554223H1 SYNONOT01 INCYTE
89 ATTAAATAGATCACCAGCTAGTTTCAGAGTTACCATGTACGTATTCCACTAGCTGGGTTCTG
90 TATTTTCAGTTCTTTTCGATACGGCTTAGGGTAATGTCAGTACAGGAAAAAACTGTGCAAGTG
91 AGCACCTGATTCCGTTGCCTTGGCTTAACTCTAAAGCTCCATGTCCTGGGCCTAAAATCGTA
92 TAAAATCTGGATTTTTTTTNTTTTTTTTTTGCGCATATTCACATATGTAAACCAGNACATTCTA
93 TGTACNACAAACCTGGTTTTTTAAAAAGGAAC
94 >4507477H1 OVARTDT01 INCYTE
95 GGCTAGTTTCAGAGTTACCATGTACGTATTCCACTAGCTGGGTTCTGTATTTTCAGTTCTTTC
96 GATACGGCTTAGGGTAATGTCAGTACAGGAAAAAACTGTGCAAGTGAGCACCTGATTCCGT
97 TGCCTTGCTTAACTCTAAAGCTCCATGTCCTGGGCCTAAAATCGTATAAAATCTGGA
98 >4163378H1 BRSTNOT32 INCYTE
99 AATAGATCACCAGCTAGTTTCAGAGTTACCATGTACGTATTCCACTAGCTGGGNTCTGTATT
100 TCAGTTCCTTTTCGATACGGCTTAGGGTAATGTCAGTACAGGAAAAAAGCTGTGCAAGTGAGC
101 ACCTGATTCCGTTGCCTTGCTTAACTCTAAAGCTCCATGTCCTGGGCCTAAAATCGTATA

Fig. 14-3



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1 >2054675H1 BEPINOT01 INCYTE
2 AAAGGAACTATGTTGCTATGAATTAACTTGTGTCGTGCTGATAGGACAGACTGGATTTTTCA
3 TATTTCTTATTAAAATTTCTGCCATTTAGAAGAAGAGAACTACATTCATGGTTTGGAAGAGAT
4 AAACCTGAAAAGAAGAGTGGCCTTATCTTCACTTTATCGATAAGTCAGTTTATTTGTTTCATT
5 GTGTACATTTTTATATTCTCCTTTTGACATTATAACTGTTGGCTTTTCTAATCTTGTTAAATA
6 TATCTATTTTTTACCAAAGGTATTTAATATTCTTTTTTA
7 >3993180H1 LUNGNON03 INCYTE
8 CACAAATCACTCACCGACGTGGCCCTGGAGCACCATGAGGNGTGTGACTGTGTGTGCAGAGGG
9 AGCACAGGAGGATAGCCGCATCACCACCAGCAGCTCTTGCCCAGAGCTGTGCAGTGCAGTGGC
10 TGATTCTATTAGAGAACGTATGCGTTATCTCCATCCTTAATCTCAGTTGTTTGCTTCAAGGAC
11 CTTTCATCTTCAGGATTTACAGTGCATTCTGAAAGAGGAGACATCAAACAGAATTAGGAGTTG
12 TGCAACAGCTCTTTTGAGAGGAGGCTAAAGGACAGGAGAAAGGTCTT
13 >3510192H1 CONCNOT01 INCYTE
14 TGCAGTGCAGTGGCTGATTCTATTAGAGAACGTATGCGTTATCTCCATCCTTAATCTCAGTTG
15 TTTGCTTCAAGGACCTTTCATCTTCAGGATTTACAGTGCATTCTGAAAGAGGAGACATCAAAC
16 AGAATTAGGAGTTGTGCAACAGCTCTTTTGAGAGGAGGCTAAAGGACAGGAGAAAAGGTCTT
17 CAATCGTGGAAAGAAAATTAAATGTTGTATTAAATAGATCACCAGCTAGTTTCAGAGTTACCA
18 TGTACGTATTCCACTAGCTGGGTTCTGTATTT
19 >4164633H1 BRSTNOT32 INCYTE
20 CTTGTAAATATATCTATTTTTTACCAAAGGTATTTAATATTCTTTANTTATGACAACTTAGAT
21 CAACTATTTTTTAGCTTGGTAAATTTTCTAAACACAAATTGTTATAGCCAGAGGAACAAAGATG
22 ATATAAAATATTGTTGCTCTGACAAAATACATGTATTTTATTCTCGTATGGTGCTAGAGTTA
23 GATTAATCTGCATTTTAAAAAACTGAATTGGAATAGAATTGGTAAGTTGCAAAGACTTTTTTGA
24 NAATAATTAAATTATCATATCTTCCATTCTCTGTTATTGGGGGAGAAAAAT
25 >2559870H1 ADRETUT01 INCYTE
26 CACGAGGTCCTTCAGTTGAGACCAAAGACCGGTGTCAGGGGATTGCACAAATCACTCACCGAC
27 GTGGCCCTGGAGCACCATGAGGAGTGTGACTGTGTGTGCAGAGGGAGCACAGGGGGATAGCCG
28 CATCACCACCAGCAGCTCTTGCCCAGAGCTGTGCAGTGCAGTGGCTGATTCTATTAGAGAACG
29 TATGCGTTATCTCCATCCTTAATCTCAGTTGTTTGCTTCAAGGACCTTTCATCTTCAGGATTT
30 ACAGTGCATTCTGAAAGAGGAGA
31 >3817470H1 BONSTUT01 INCYTE
32 TTAAAAAGGAACTATGTTGCTATGAATTAACTTGTGTCATGCTGATAGGACAGACTGGATTT
33 TTCATATTTCTTATTAAAATTTCTGCCATTTAGAAGAAGAGAACTACATTCATGGTTTGGAAG
34 AGATAAACCTGAAAAGAAGAGTGGCCTTATCTTCACTTTATCGATAAGTCAGTTTATTTGTTT
35 CATTGTGTACATTTTTATATTCTCCTTTTGACATTATAACTGTTGGCTTTCTAATCTGTTAAA
36 TATATCTATTTTTTACCAAAGGTATTTAATATTCTTT
37 >3979767H1 LUNGTUT08 INCYTE
38 GGAGGATAGCCGCATCACCACCAGCAGCTCTTGCCCAGAGCTGTGCAGTGCAGTGGCTGATTC
39 TATTAGAGAACGTATGCGTTATCTCCATCCTTAATCTCAGTTGTTTGCTTCAAGGACCTTTCA
40 TCTTCAGGATTTACAGTGCATTCTGAAAGAGGAGACATCAAACAGAATTAGGAGTTGTGCAAC
41 AGCTCTTTTGAGAGGAGGCTAAAGGACAGGAGAAAAGGTCTTCAATCGTGGAAAGAAATTA
42 AATGTTGTATTAAATAGACACCAGCT

Fig. 15-1



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43 >3980011H1 LUNGTUT08 INCYTE
44 GGAGGATAGCCGCATCACCACCAGCAGCTCTTGCCAGAGCTGTGCAGTGCAGTGGCTGATTC
45 TATTAGAGAACGTATGCGTTATCTCCATCCTTAATCTCAGTTGTTTGCTTCAAGGACCTTTCA
46 TCTTCAGGATTTACATGCATTCTGAAAGAGGAGACATCAAACAGAATTAGGAGTTGTGCAACA
47 GCTCTTTTGAGAGGAGGCCTAAAGGACAGGAGAAAAGGTCTTCAATCGTGGAAGAAAATTAA
48 ATGTTGTATTAAATAGATCACCA
49 >4825396H1 BLADDIT01 INCYTE
50 GAGAACCGATACCATTTTTCTGGCCAGGTTGTCTCCTGGTTAAACGCTGTGGTGGGAAGTGTGC
51 CTGTTGTCTCCACAATTGCAATGAATGTCAATGTGTCCCAAGCAAAGTTACTAAAAAATACCA
52 CGAGGTCTTTCAGTTGAGACCAAAGACCGGTGTGAGGGGATTGCACAAATCACTCACCAGCGT
53 GGCCCTGGAGCACCATGAGGAGTGTGACTGTGTGTGCAGAGGGAGCACAGGAGGATAGCCGCA
54 TCACCACCA
55 >30737003H1 BONEUNT01 INCYTE
56 AGAAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGGAGGTAAGATTATACAGCTGCACA
57 CCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATACCATTTTTCTGGCCA
58 GGTGTGTCTCCTGGTTAAACGCTGTGGTGGGAAGTGTGCCTGTTGTCTCCACAATTGCAATGAA
59 TGTCAATGTGTCCCAAGCAAAGTTACTAAAAAATACCACGAGGTCCTTCAGTTGAGACCAAAG
60 ACCGGTGTGAGGGGATTGCACAAATCA
61 >862169H1 BRAITUT03 INCYTE
62 AGATGATATAAAATATTGTTGCTCTGACAAAAATACATGTATTTTATTCTCGTATGGTGCTAG
63 AGTTAGATTAACTGCAATTTTAAAAAAGTGAATTGGAATAGAATTGGTAAGTTGCAAAGACTT
64 TTTGAAAATAATTAAATTATCATATCTTCCATTCTGTTATTGGAGATGAAAATAAAAAGCAA
65 CTTATGAAAGTAGACATTCAGATCCAGCCATTACTAACCTATTCTTTTTTTGGGGAAATCTGA
66 GCCTAGC
67 >4201385H1 BRAITUT29 INCYTE
68 TTTTTTAAAAGGAAGTATGTTGCTATGAATTAACTTGTGTGCTGCTGATAGGACAGACTGGA
69 TTTTTTCATATTTCTTATTAAATTTCTGCCATTTAGAAGAAGAGAACTACATTCATGGTTTGG
70 AAGAGATAAACCTGAAAAGAAGAGTGGCCTATCTTCACTTTATCGATAAGTCAGTTTATTTGT
71 TTCATTGTGTACATTTTTTATATTCTCCTTTGACATATACTGTTGGCTTTTCTAATCTGTTAA
72 ATATATCTATTTTTTACCAAAGGTATTTAATAT
73 >1302516H1 PLACNOT02 INCYTE
74 AGGAAATCAAATTAGGATAAGATTTGTATCTGATGAATATTTTCTTCTGAACCTTCTAACAG
75 AGGAGGTAAGATTATACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTAA
76 AGAGAACCGATACCATTTTTCTGGCCAGGTTGTCTCCTGGTTAAACGCTGTGGTGGGAAGTGTG
77 CCTGTTGTCTCCCACAATTGCAATGAATGTCAATGTGTCCCAAGCAAAGTTACTAAAAAATAC
78 CACGAGGTCC
79 >3684109H1 HEANOT01 INCYTE
80 ATTTTCATCTTCAGGATTTACAGTGCATTCTGAAANAGGAGAAATCAAACANAATTAGGAGTTG
81 TGCAACAGCTCTTTTGAGAGGAGGCCTAAAGGACAGGAGAAAAGGTCTTCAATCGTGGAANA
82 AAATTAAATGTTGTATTAAATAGATCACCAGCTAGTTTCAGAGTTACCATGTACGTATTCCAC
83 TAGCTGGGTTCTGTATTTTCAGTTCTTTGATACGGCTTAGGGTAATGTCAGTACAGGAAAAAA
84 ACTGTGCAAGTGAGCACCTGATTCCGTTGCCTTGCTT

Fig. 15-2



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85 >2549720H1 LUNGTUT06 INCYTE
86 TTAGCTTGGNAAATTTTCTAAACACAATTGTTATAGCCAGAGGAACAAAGATGATATAAAAT
87 ATTGTTGCTCTGACAAAATACATGTATTTTCATTCTCGTATGGTGCTAGAGTTAGATTAATCT
88 GCATTTTAAAAAACTGAATTGGAATAGAATTGGTAAGTTGCAAAGACTTTTTGAAAATAATTA
89 AATTATCATATCTTCCATTCTGTTATTGGAGATGAAAATAAAAAGCAACTTATGANAGTAG
90 >877279H1 LUNGAST01 INCYTE
91 CTTTTTTATGACAACTTAGATCAACTATTTTGTAGCTTGGTAAATTTTCTAAACACAATTGTT
92 ATAGCCAGAGGAACAAAGATGATATAAAATATTGTTGCTCTGACAAAATACATGTATTTTCAT
93 TCTCGTATGGTGCTAGAGTTAGATTAATCTGCATTTTAAAAAACTGAATTGGAATAGAATTGG
94 TAAGTTGCAAAGGCTTTTTGAAAATAATTAAATTATCATATCTTCCATTCTGTTATTGGNGG
95 >4713188H1 BRAIHCT01 INCYTE
96 CAAAGTTACTAAAAATACCACGAGGTCCTTCAGTTGAGACCAAAGACCGGTGTCAGGGGATT
97 GCACAAATCACTCACCGACGTGGCCCTGGAGCACCATGAGGAGTGTGACTGTGTGTGCAGAGG
98 GAGCACAGGAGGATAGCCGCATCACCACCAGCAGCTCTGCCCAGAGCTGTGCAGTGCAGTGG
99 CTGATTCTATTAGAGAACGTATGCGTTATCTCCATCCTTAATCTCAGTTGTTTGCT
100 >2171082H1 ENDCNOT03 INCYTE
101 AGATAAACCTGAAAAGAAGAGTGGCCTTATCTTCACTTTATCGATAAGTCAGTTTATTTGTTT
102 CATTGTGTACATTTTTATATTCTCCTTTTGACATTATAACTGTTGGCTTTTCTAATCTTGTTA
103 AATATATCTATTTTTACCAAAGGTATTTAATATTCTTTTTTATGACAACCTTAGATCAACTATT
104 TTTAGCTTGGTAAATTTTCTAAACACAATTGTTATAGCCAGAGGAACAAAGATGA
105 >875860H1 LUNGAST01 INCYTE
106 CTGGATTTTTTCATATTTCTTATTAAATTTCTGCCATTTAGAAGAAGAGAACTACATTCATGG
107 TTTGGAAGAGATAAACCTGAAAAGAAGAGTGGCCTTATCTTCACTTTATCGATAAGTCAGTTT
108 ATTTGTTTCATTGTGTACATTTTATATTCTCCTTTTGACATTATAACTGTTGGCTTTTCTAAT
109 CTTGTTAAATATATCTATTTTTACCAAAGGTATTTAATATTCTTTTTTTATGAC
110 >706168H1 SYNORAT04 INCYTE
111 GCTCATATTCACATATGTAAACCAGAACATTCTATGTACTACAAACCTGGTTTTTAAAAAGGA
112 NCTATGTTGCTATGAATTAACTTGTGTCTGTGCTGATAGGACAGACTGGATTTTTCATATTTT
113 TTATTAAAATTTCTGCCATTTAGAAGAAGAGAACTACATTCATGGTTTGAAGAGATAAACCT
114 GAAAAGAAGAGTGGCCTTATCTTCANTTTATCGATAAGTCAGTTTATTTGTTTCA
115 >458823H1 KERANOT01 INCYTE
116 ANGAGTTGCCCAGAGCTGTGCAGTGCAGTGGCTGATTCTATTAGAGAACGTATGCGTTATCTC
117 CATCCTTAATCTCAGTTGTTTGNNTCAAGGACCTTTCATCTTCAGGATTTACAGTGCATTCTG
118 AAAGAGGAGACATCAAACAGAATTAGGAGTTGTGCAACAGCTCTTTTGAGAGGAGGCCTAAAG
119 GNCAGGAGAAAAGGTCTTCAATCGTGAAAGAAAATTAATGTTGTATTAAATAGATC
120 >538436H1 LNODNOT02 INCYTE
121 AAAGATGATATAAAATATTGTTGCTCTGACAAAATACATGTATTTTCATTCTCGTATGGTGCT
122 AGAGTTAGATTAATCTGCATTTTAAAAAACTGAATTGGAATAGAATTGGTAAGTTGCAAAGAC
123 TTTTTGAAAATAATTAAATTATCATATCTTCCATTCTGTTATTGGAGATGAAAATAAAAAGC
124 AACTTATGAAAGTAGACATTCAGATCCAGCCATTACTAACCTAT

Fig. 15-3



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125 >1303909H1 PLACNOT02 INCYTE
126 AGGAAATCAAATTAGGATAAGATTTGTATCTGATGAATATTTTCCTTCTGAACCTTCTAACAG
127 AGGAGGTAAGATTATACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTAA
128 AGAGAACCGATACCATTTTCTGGCCAGGTTGTCTCCTGGTTAAACGCTGTGGTGGGAACGTGTG
129 CCTGTTGTCTCCACAATTGCAATGAATGTCAATGTGTCCCAAG
130 >2739211H1 OVARNOT09 INCYTE
131 GTGCATTCTGAAAGAGGAGACATCAAACAGAATTAGGAGTTGTGCAACAGCTCTTTTGAGAGG
132 AGGCCTAAAGGACAGGAGAAAAGGTCTTCAATCGTGGAAGAAAATTAAATGTTGTATTAAAT
133 AGATCACCAGCTAGTTTCAGAGTTACCATGTACGTATTCCACTAGCTGGGTTCTGTATTTCAG
134 TTCTTTCGATACGGCTTAGGGTAATGTCAGTACAGGAAAAAACTGTGCAAGTGAGCACCTGA
135 T
136 >2550343H1 LUNGTUT06 INCYTE
137 TGTACATTTTTATATTCTCCTTTTGACATTATAACTGTTGGCTTTTCNAATCTTGTTAAATAT
138 ATCTATTTTTTACCAAAGGTATTTAATATTCTTTTTTATGACAACTTAGATCAACTATTTTTAG
139 CTTGGTAAATTTTTCTAAACACAATTGTTATAGCCAGAGGAACAAAGATGATATAAAATATTG
140 TTGCTCTGACAAAAATACATGTATTTTCAATCTCGTATGGTGCTA
141 >5321148H1 FIBPFEN06 INCYTE
142 CACAATTGTTATAGCCAGAGGAACAAAGATGATATAAAATATTGTTGCTCTGNCAAAAAATACA
143 TGTATTTTCATTCTCGTATGGTGCTAGAGTTAGATTAATCTGCATTTTAAAAAACTGAATTGGA
144 ATAGAATTGGTAAGTTGCAAAGACTTTTTGAAAATAATTAAATTATCATATCTTCCATTCTCTG
145 TTATTGGAGATGAAAATAAAAAAGCAACTTATGAAAGTAAATTCAGATCCACCATTACTAAC
146 >879495H1 THYRNOT02 INCYTE
147 ATTTCAATCTCGTATGGTGCTAGAGTTAGATTAATCTGCATTTTAAAAAACTGAATTGGAATA
148 GAATTGGTAAGTTGCAAAGACTTTTTGAAAATAATTAAATTATCATATCTTCCATTCTCTGTTA
149 TTGGAGATGAAAATAAAAAAGCAACTTATGAAAGTAGACATTCAGATCCAGCCATTACTAACCT
150 ATTCCTTTTTTTGGGGAAATCTGAGCCTAGCTCAGAAAAACATAAAGCACCTTGAAAAA
151 >3325591H1 PTHYNOT03 INCYTE
152 TGCAACAGCTCTTTTGAGAGGAGGCCTAAAGGACAGGAGAAAAGGTCTTCAATCGTGGAAGA
153 AAATTAAATGTTGTATTAAATAGATCACCAGCTAGTTTCAGAGTTACCATGTACGTATTCCAC
154 TAGCTGGGTTCTGTATTTTCAAGTTCTTTCGATACGGCTTAGGGTAATGTCAGTACAGGAAAAA
155 ACTGTGCAAGTGAGCACCTGATTCCGTTGCCTTGCTTAACCCCTAAAGCNCCATGTCNNGGGCN
156 AAAANCGAAAAAT
157 >543890H1 OVARNOT02 INCYTE
158 TTTCTAAACACAATTGTTATAGCCAGAGGAACAAAGATGATATAAAATATTGTTGCTCTGACA
159 AAAATACATGTATTTTCAATCTCGTATGGTGCTAGAGTTAGATTAATCTGCATTTTAAAAAACT
160 GAATTGGNATAGAATTGGTAAGTTGCAAAGNCTTTTTGAAAATAATTAAATTATCATATCTTC
161 CATTCTGTATTGAGGATGGAAAATAAAAAAGCAACTTATGGAAAGTAGGACATTTCAGATC
162 >3733565H1 SMCCNOS01 INCYTE
163 CCTTAATCTCAGTTGTTTGCTTCAAGGACCTTTTCATCTTCAGGATTTACAGTGCATTCTGNAA
164 GANGAGACATCAAACAGAATTAGGNGTTGTGCAAAAGCTCTTTTGAGAGGAGGCCTAAAGGAC
165 AGGAGAAAAGGTCTNCAATCGTGGAAGNAAATTAAATGTTGTATNAAATNGATCACCAGCTA
166 GTTTCAGAGTTACCATGTACGTATTCCACTAGCTGGGNCNGTATTTCAGTCTTTCGGAACGGCT
167 TAGGGTAATGTCAGTACAGGANAAAACTGTGCAGTGAG

Fig. 15-4



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254 >3732621H1 SMCCNOS01 INCYTE
255 ANAGATGATATAAAANATTGTTGCTCTGACAANNATACATGTATTTTCATTCTCGTATGGTGCT
256 AGAGTTAGATTAATCTGCNTTTTAAAAAACTGANTTGAATAGANTTGGTAAGTTGCAAAGNC
257 NTTTGAAAATNATTAAGTTATCAGAT
258 >3530274H1 BLADNOT09 INCYTE
259 TTCCATTCTGTTATTGGAGATGAAAATAAAAAGCAACTTATGAAAGTAGACATTCAGATCCA
260 GCCATTACTAACCTATTCCTTTTTTGGGGAAATCTGAGCCTAGCTCAGAAAAACATAAAGCAC
261 CTTGAAAAAGACTTGGCAGCTTCCTGATAAAGCGTGCTGTGCTGTGCAGTAGGAACACATCCT
262 ATTTATTGTGATGTTGTGGTTTTATTATCTAAACTCTGTTCCATACACTTGTATAAATACATG
263 GATATTTTTATGTACAGAAGTATGTCTCTTAACCAGTTCA
264 >3530249H1 BLADNOT09 INCYTE
265 CTTCCATTCTGTTATTGGAGATGAAAATAAAAAGCAACTTATGANAGTAGACATTCAGATCC
266 AGCCATTACTAACCTATTCCTTTTTTGGGGAAATCTGAGCCTAGCTCAGAAAAACATAAAGCA
267 CTTGAAAAAGACTTGGCAGCTTCCTGATAAAGCGTGCTGTGCTGTGCAGTAGGAACACATCC
268 TATTTATTGTGATGTTGTGGTTTTATTATCTTAAACTCTGTTCCATACACTTGTATAAATACA
269 TGGATATTTTTATGTACAGAAGTATGTCTCTTAACCAGTTCACTTATTGTACCTGG

Fig. 15-7



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VEGFE1	AAAATGTATGGATACAACTTAC	22
VEGFE2	GTTTGATGAAAGATTTGGGCTTG	23
VEGFE3	TTTCTAAAGGAAATCAAATTAG	22
VEGFE4	GATAAGATTTGTATCTGATG	20
VEGFE5	GATGTCTCCTCTTTTCAG	17
VEGFE6	GCACAACTCCTAATTCTG	18
VEGFE7	AGCACCTGATTCCGTTGC	19
VEGFE8	TAGTACATAGAATGTTCTGG	20
VEGFE9	AAGAGACATACTTCTGTAC	19
VEGFE10	CCAGGTACAATAAGTGAAGTGA	21

Fig. 16



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+3           M N I F L L N L L T E E V R L Y
              ]-----
1  AGGAAATCAA ATTAGGATAA GATTGTATC TGATGAATAT TTTCCTTCTG AACCTTCTAA CAGAGGAGGT AAGATTATAC
   TCCTTTAGTT TAATCCTATT CTAAACATAG ACTACTTATA AAAGGAAGAC TTGGAAGATT GTCTCCTCCA TTCTAATATG

+3  S C T P R N F S V S I R E E L K R T D T I F W P G C L
      -----]-----
81  AGCTGCACAC CTCGTAAC TTCTAGTGTCC ATAAGGGAAG AACTAAAGAG AACCGATACC ATTTTCTGGC CAGGTTGTCT
   TCGACGTGTG GAGCATTGAA GAGTCACAGG TATTCCCTTC TTGATTCTC TTGGCTATGG TAAAGACCG GTCCAACAGA
-2                                     <-----

+3  L V K R C G G N C A C C L H N C N E C Q C V P S K V
      -----
161 CCTGGTTAAA CGCTGTGGTG GGAAGTGTGC CTGTTGTCTC CACAATTGCA ATGAATGTCA ATGTGTCCCA AGCAAAGTTA
   GGACCAATTT GCGACACCAC CCTTGACACG GACAACAGAG GTGTTAACGT TACTTACAGT TACACAGGGT TCGTTTCAAT
-2 -----

+3  T K K Y H E V L Q L R P K T G V R G L H K S L T D V A
      -----
+1                                     V S G D C T N H S P T W P
                                      ]-----
241 CTAAAAATA CCACGAGGTC CTTCAAGTGA GACCAAAGAC CGGTGTCAGG GGATTGCACA AATCACTCAC CGACGTGGCC
   GATTTTTTAT GGTGCTCCAG GAAGTCAACT CTGGTTTCTG GCCACAGTCC CCTAACGTGT TTAGTGAGTG GCTGCACCGG
-2 -----[

+3  L E H H E E C D C V C R G S T G G
      ----->
+2                                     V Q R E H R R I A A S P P A A L A
                                      ]-----
+1  W S T M R S V T V C A E G A Q E D S R I T T S S S C
      -----
321 CTGGAGCACC ATGAGGAGTG TGACTGTGTG TGCAGAGGGA GCACAGGAGG ATAGCCGCAT CACCACCAGC AGCTCTTGCC
   GACCTCGTGG TACTCCTCAC ACTGACACAC ACGTCTCCCT CGTGTCTCTC TATCGGCGTA GTGGTGGTCG TCGAGAACGG

+2  Q S C A V Q W L I L L E N V C V I S I L N L S C L L Q
      -----
+1  P E L C S A V A D S I R E R M R Y L H P
      ----->
401 CAGAGCTGTG CAGTGCAGTG GCTGATTCTA TTAGAGAACG TATGCGTTAT CTCCATCCTT AATCTCAGTT GTTTGCTTCA
   GTCTCGACAC GTCACGTCAC CGACTAAGAT AATCTCTTGC ATACGCAATA GAGGTAGGAA TTAGAGTCAA CAAACGAAGT
```

Fig. 17-1



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+2 G P F I F R I Y S A F
----->

481 AGGACCTTTC ATCTTCAGGA TTTACAGTGC ATTCTGAAAG AGGAGACATC AAACAGAATT AGGAGTTGTG CAACAGCTCT
TCCTGGAAAG TAGAAGTCCT AAATGTCACG TAAGACTTTC TCCTCTGTAG TTTGTCTTAA TCCTCAACAC GTTGTGCGAGA

561 TTTGAGAGGA GGCCTAAAGG ACAGGAGAAA AGGTCTTCAA TCGTGGAAG AAAATTAAAT GTTGTATTAA ATAGATCACC
AAACTCTCCT CCGGATTTC TGTCTCTTT TCCAGAAGTT AGCACCTTTC TTTTAATTTA CAACATAATT TATCTAGTGG

641 AGCTAGTTTC AGAGTTACCA TGTACGTATT CCACTAGCTG GGTCTGTAT TTCAGTTCTT TCGATACGGC TTAGGGTAAT
TCGATCAAAG TCTCAATGGT ACATGCATAA GGTGATCGAC CCAAGACATA AAGTCAAGAA AGCTATGCCG AATCCCATT

721 GTCAGTACAG GAAAAAACT GTGCAAGTGA GCACCTGATT CCGTTGCCTT GGCTTAACTC TAAAGCTCCA TGTCTGGGC
CAGTCATGTC CTTTTTTTGA CACGTTCACT CGTGGAATAA GGCAACGGAA CCGAATTGAG ATTTGAGGT ACAGGACCCG

801 CTAAAATCGT ATAAAATCTG GA
GATTTTAGCA TATTTTAGAC CT

Fig. 17-2



VASCULAR ENDOTHELIAL GROWTH
FACTOR-X
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```
+3          M N I F L L N L L T E E V R L Y
          ]-----
1  AGGAAATCAA ATTAGGATAA GATTGTATC TGATGAATAT TTCCTTCTG AACCTTCTAA CAGAGGAGGT AAGATTATAC
   TCCTTTAGTT TAATCCTATT CTAAACATAG ACTACTTATA AAAGGAAGAC TTGGAAGATT GTCTCCTCCA TTCTAATATG

+3  S C T P R N F S V S I R E E L K R T D T I F W P G C L
   -----]-----
81 AGCTGCACAC CTCGTAACCT CTCAGTGTCC ATAAGGGAAG AACTAAAGAG AACCGATACC ATTTTCTGGC CAGGTTGTCT
   TCGACGTGTG GAGCATTGAA GAGTCACAGG TATTCCTTC TTGATTCTC TTGGCTATGG TAAAGACCG GTCCAACAGA
-2          <-----

+3  L V K R C G G N C A C C L H N C N E C Q C V P S K V
   -----
161 CCTGGTTAAA CGCTGTGGTG GGAAGTGTGC CTGTTGTCTC CACAATTGCA ATGAATGTCA ATGTGTCCCA AGCAAAGTTA
   GGACCAATTT GCGACACCAC CCTTGACACG GACAACAGAG GTGTTAACGT TACTTACAGT TACACAGGGT TCGTTTCAAT
-2 -----

+3  T K K Y H E V L Q L R P K T G V R G L H K S L T D V A
   -----
+1          V S G D C T N H S P T W P
          ]-----
241 CTAAAAAATA CCACGAGGTC CTTAGTTGA GACCAAAGAC CGGTGTCAGG GGATTGCACA AATCACTCAC CGACGTGGCC
   GATTTTTTAT GGTGCTCCAG GAAGTCAACT CTGGTTTCTG GCCACAGTCC CCTAACGTGT TTAGTGAGTG GCTGCACCGG
-2 -----[

+3  L E H H E E C D C V C R G S T G G
   ----->
+2          V Q R E H R R I A A S P P A A L A
          ]-----
+1  W S T M R S V T V C A E G A Q E D S R I T T S S S C
   -----
321 CTGGAGCACC ATGAGGAGTG TGAAGTGTG TGCAGAGGGA GCACAGGAGG ATAGCCGCAT CACCACCAGC AGCTCTTGCC
   GACCTCGTGG TACTCCTCAC ACTGACACAC ACGTCTCCCT CGTGTCTCTC TATCGGCGTA GTGGTGGTCG TCGAGAACGG

+2  Q S C A V Q W L I L L E N V C V I S I L N L S C L L Q
   -----
+1  P E L C S A V A D S I R E R M R Y L H P
   ----->
401 CAGAGCTGTG CAGTGCAGTG GCTGATTCTA TTAGAGAACG TATGCGTTAT CTCCATCCTT AATCTCAGTT GTTTGCTTCA
   GTCTCGACAC GTCACGTCAC CGACTAAGAT AATCTCTTGC ATACGCAATA GAGGTAGGAA TTAGAGTCAA CAAACGAAGT
```

Fig. 18-1



VASCULAR ENDOTHELIAL GROWTH
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+2 G P F I F R I Y S A F
----->

481 AGGACCTTTC ATCTTCAGGA TTTACAGTGC ATTCTGAAAG AGGAGACATC AAACAGAATT AGGAGTTGTG CAACAGCTCT
TCCTGGAAAG TAGAAGTCCT AAATGTCACG TAAGACTTTC TCCTCTGTAG TTTGTCTTAA TCCTCAACAC GTTGTGCGAGA

561 TTTGAGAGGA GGCCTAAAGG ACAGGAGAAA AGGTCTTCAA TCGTGGAAAG AAAATTAAAT GTTGATTAA ATAGATCACC
AAACTCTCCT CCGGATTTCC TGTCTCTTT TCCAGAAATT AGCACCTTTC TTTTAATTTA CAACATAATT TATCTAGTGG

641 AGCTAGTTTC AGAGTTACCA TGTACGTATT CCACTAGCTG GGTCTGTAT TTCAGTTCTT TCGATACGGC TTAGGGTAAT
TCGATCAAAG TCTCAATGGT ACATGCATAA GGTGATCGAC CCAAGACATA AAGTCAAGAA AGCTATGCCG AATCCCATTA

721 GTCAGTACAG GAAAAAACT GTGCAAGTGA GCACCTGATT CCGTTGCCTT GGCTTAACTC TAAAGCTCCA TGTCTGGGC
CAGTCATGTC CTTTTTTTGA CACGTTCACT CGTGGACTAA GGCAACGGAA CCGAATTGAG ATTTGAGGT ACAGGACCCG

801 CTAAAAATCGT ATAAAAATCTG GATTTTTTTN TTTTTTTTG CGCATATTCA CATATGTAAA CCAGAACATT CTATGTACTA
GATTTTAGCA TATTTTAGAC CTAAAAAAN AAAAAAATC GCGTATAAGT GTATACATTT GGTCTGTGTA GATACATGAT

881 CAAACCTGGT TTTTAAAAAG GAACTATGTT GCTATGAATT AAACCTGTGT CGTGCTGATA GGACAGACTG GATTTTTCAT
GTTTGGACCA AAAATTTTTC CTTGATACAA CGATACTTAA TTTGAACACA GCACGACTAT CCTGTCTGAC CTAAAAAGTA

-3 <-----

961 ATTTCTTATT AAAATTTCTG CCATTAGAA GAAGAGAACT ACATTCATGG TTTGGAAGAG ATAAACCTGA AAAGAAGAGT
TAAAGAATAA TTTTAAAGAC GGTAAATCTT CTTCTCTTGA TGTAAGTACC AAACCTTCTC TATTTGGACT TTTCTTCTCA

-3 -----

1041 GGCCTTATCT TCACTTTATC GATAAGTCAG TTTATTTGTT TCATTGTGTA CATTTTATA TTCTCCTTTT GACATTATAA
CCGGAATAGA AGTGAAATAG CTATTCAGTC AAATAAACAA AGTAACACAT GTAAAAATAT AAGAGGAAAA CTGTAATATT

-3 ----- [

1121 CTGTTGGCTT TTCTAATCTT GTTAAATATA TCTATTTTTC CCAAAGGTAT TTAATATTCT TTTTATGAC AACTTAGATC
GACAACCGAA AAGATTAGAA CAATTATAT AGATAAAAAAT GGTTCCTATA AATTATAAGA AAAAATACTG TTGAATCTAG

1201 AACTATTTT AGCTTGGTAA ATTTTCTAA ACACAATTGT TATAGCCAGA GGAACAAAGA TGATATAAAA TATTGTTGCT
TTGATAAAAA TCGAACCATT TAAAAAGATT TGTGTTAACA ATATCGGTCT CCTTGTTTCT ACTATATTTT ATAACAACGA

1281 CTGACAAAAA TACATGTATT TCATTCTCGT ATGGTGCTAG AGTTAGATTA ATCTGCATTT TAAAAAATCTG AATTGGAATA
GACTGTTTTT ATGTACATAA AGTAAGAGCA TACCACGATC TCAATCTAAT TAGACGTAAA ATTTTTTGAC TTAACCTTAT

1361 GAATTGGTAA GTTGCAAAGA CTTTTTGAAA ATAATTAAAT TATCATATCT TCCATTCCTG TTATTGGAGA TGAAAAATAA
CTTAACCATT CAACGTTTCT GAAAACTTT TATTAATTTA ATAGTATAGA AGGTAAGGAC AATAACCTCT ACTTTTATTT

Fig. 18-2



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1441 AAGCAACTTA TGAAAGTAGA CATTGAGATC CAGCCATTAC TAACCTATTC CTTTTTTGGG GAAATCTGAG CCTAGCTCAG
TTCGTTGAAT ACTTTCATCT GTAAGTCTAG GTCGGTAATG ATTGGATAAG GAAAAAAGCC CTTTAGACTC GGATCGAGTC

1521 AAAACATAA AGCACCTTGA AAAAGACTTG GCAGCTTCCT GATAAAGCGT GCTGTGCTGT GCAGTAGGAA CACATCCTAT
TTTTTGATT TCGTGGAAGT TTTTCTGAAC CGTCGAAGGA CTATTTGCA CGACACGACA CGTCATCCTT GTGTAGGATA

1601 TTATTGTGAT GTTGTGGTTT TATTATCTTA AACTCTGTTC CATACACTTG TATAAATACA TGGATATTTT TATGTACAGA
AATAACACTA CAACACCAA ATAATAGAAT TTGAGACAAG GTATGTGAAC ATATTTATGT ACCTATAAAA ATACATGTCT

1681 AGTATGTCTC TTAACCAGTT CACTTATTGT ACCTGG
TCATACAGAG AATTGGTCAA GTGAATAACA TGGACC

Fig. 18-3



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DNA AND POLYPEPTIDE SEQUENCE USED FOR MAMMALIAN CELL EXPRESSION

```
+1      m s l f g l l l l t s a l a g q r
1      GGATCCAAAA TGAGCCTCTT CGGGCTTCTC CTGCTGACAT CTGCCCTGGC CGGCCAGAGA

+1      q g t q a E S N L S S K F Q F S S N K E
61     CAGGGGACTC AGGCGGAATC CAACCTGAGT AGTAAAGTTC CAGTTTTCCA GCAACAAGGA

+1      Q N G V Q D P Q H E R I I T V S T N G S
121    ACAGAACGGA GTACAAGATC CTCAGCATGA GAGAATTATT ACTGTGTCTA CTAATGGAAG

+1      I H S P R F P H T Y P R N T V L V W R L
181    TATTCACAGC CCAAGGTTTC CTCATACTTA TCCAAGAAAT ACGGTCTTGG TATGGAGATT

+1      V A V E E N V W I Q L T F D E R F G L E
241    AGTAGCAGTA GACGAAAATG TATGGATACA ACTTACGTTT GATGAAAGAT TTGGGCTTGA

+1      D P E D D I C K Y D F V Z V E E P S D G
301    AGACCCAGAA GATGACATAT GCAAGTATGA TTTTGTAGAA GTTGACAAAC CCAGTGATGG

+1      T I L G R W C G S G T V P G K Q I S K G
361    AACTATATTA GGGCCCTGGT GTGGTTCTGG TACTGTACCA GGAAAACAGA TTTCTAAAGG

+1      N Q I R I R F V S D E Y F P S E P G F C
421    AAATCAAATT AGGATAAGAT TTGTATCTGA TGAATATTTT CCTTCTGPAC CAGGGTTCTG

+1      I H Y N I V M P Q F T E A V S P S V L P
481    CATCCACTAC AACATTGTCA TGCCACAATT CACAGAAGCT GTGAGTCCTT CAGTGCTACC

+1      P S A L P L D L L N N A I T A F S T L E
541    CCCTTCAGCT TTGCCACTTG GACCTGCTTA ATAATGCTAT AACTGCCTTT AGTACCTTCG

+1      D L I R Y L E P E R W Q L D L E D L Y R
601    AAGACCTTAT TCGATATCTT GAACCAGAGA GXTGGCAGTT GGACTTAGAA GATCTATATA

+1      P T W Q L L G K A F V F G R K S R V V D
661    GGCCAACTTG GCAACTTCTT GGCAAGGCTT TTGTTTTTGG AAGAAAATCC AGAGTGGTGG

+1      L N L L T E E V R L Y S C T P R N F S V
721    ATCTGAACCT TCTAACAGAG GAGGTAAGXT TATACAGCTG CACACCTCGT AACTTCTCAG

+1      S I R E E L K R T D T I F W P G C L L V
781    TGTCCATAAG GGAAGAACTT AAAGAGAACC GATACCATTT TCTGGCCAGG TTGTCTCCTG
```

Fig. 19-1



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+1 K R C G G N C A C C L H N C N E C Q C V
841 GTTAAACGCT GTGGTGGGAA CTGTGCCTGT TGTCTCCACA ATTGCAATGA ATGTCAATGT

+1 P S K V T K K Y H E V L Q L R P K T G V
901 GTCCCAAGCA AAGTTACTAA AAAATACCAC GAGGTCCTTC AGTTGAGACC AAAGACCGGT

+1 R G L H K S L T D V A L E H H E E C G C
961 GTCAGGGGAT TGCACAAATC ACTCACCGAC GTGGCCCTGG AGCACCATGA GGAGTGTGAC

+1 V C R G S T G G S R G P F E C K P I P N
1021 TGTGTGTGCA GAGGGAGCAC AGGAGGATCT AGAGGGCCCT TCGAAGGTAA GCCTATCCCT

+1 P L L G L D S T R T G H H H H H H
1081 AACCTCTCC TCGGTCTCGA TTCTACGCGT ACCGGTCATC ATCACCATCA CCATTGA

Fig. 19-2



VASCULAR ENDOTHELIAL GROWTH
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DNA AND POLYPEPTIDE SEQUENCE USED FOR BACULOVIRUS/INSECT CELL EXPRESSION

1 GAATTCAAAG GCCTGTATTT TACTGTTTTT GTAACAGTTT TGTAATAAAA AAACCTATAA
+3 m k f l v n v a l v f m v v y i s y i
61 ATATGAAATT CTTAGTCAAC GTTGCCCTTG TTTTATGGT CGTATACATT TCTTACATCT
+3 y a D P E S H H H H H E S N L S S K F
121 ATGCGGATCC GGAGTCTCAC CATCACCACC ATCATGAATC CAACCTGAGT AGTAAATTCC
+3 Q F S S N K E Q N G V Q D P Q H E R I I
181 AGTTTTCCAG CAACAAGGAA CAGAACGGAG TACAAGATCC TCAGCATGAG AGAATTATTA
+3 T V S T N G S I H S P R F P H T Y P R N
241 CTGTGTCTAC TAATGGAAGT ATTCACAGCC CAAGGTTTCC TCATACTTAT CCAAGAAATA
+3 T V L V W R L V A V E E N V W I Q L T F
301 CGGTCTTGGT ATGGAGATTA GTAGCAGTAG AGGAAAATGT ATGGATACAA CTTACGTTTG
+3 D E R F G L E D P G D D I C K Y D F V G
361 ATGAAAGATT TGGGCTTGAA GACCCAGAAG ATGACATATG CAAGTATGAT TTTGTAGAAG
+3 V E E P S D G T I L G R W C G S G T V P
421 TTGAGGAACC CAGTGATGGA ACTATATTAG GGCGCTGGTG TGGTCTGGT ACTGTACCAG
+3 G K E I S K G N Q I R I R F V S D E Y F
481 GAAAACAGAT TTCTAAAGGA AATCAAATTA GGATAAGATT TGTATCTGAT GAATATTTTC
+3 P S E P G F C I H Y N I V M P Q F T E A
541 CTTCTGAACC AGGGTTCTGC ATCCACTACA ACATTGTCAT GCCACAATTC ACAGAAGCTG
+3 V S P S V L P P S A L P L D L L N N A I
601 TGAGTCCTTC AGTGCTACCC CCTTCAGCTT TGCCACTGGA CCTGCTTAAT AATGCTATAA
+3 T A F S T L E D L I R Y L E P E R W Q L
661 CTGCCTTTAG TACCTTGGAA GACCTTATTC GATATCTTGA ACCAGAGAGA TGGCAGTTGG
+3 D L E D L Y R P T W Q L L G K A F V F G
721 ACTTAGAAGA TCTATATAGG CCAACTTGGC AACTTCTTGG CAAGGCTTTT GTTTTTTGAA

Fig. 20-1



VASCULAR ENDOTHELIAL GROWTH
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+3 R K S R V V D L R L L T E E V R L Y S C
781 GAAAATCCAG AGTGGTGGAT CTGAACCTTC TAACAGAGGA GGTAAGATTA TACAGCTGCA

+3 T P R N F S V S I R E E L K R T D T I F
841 CACCTCGTAA CTTCTCAGTG TCCATAAGGG AAGAACTAAA GAGAACCGAT ACCATTTTCT

+3 W P G C L L V K R C G G N C A C C L H N
901 GGCCAGGTTG TCTCCTGGTT AAACGCTGTG GTGGGAACTG TGCCTGTTGT CTCCACAATT

+3 C N E C Q C V P S K V T K K Y H E V L Q
961 GCAATGAATG TCAATGTGTC CCAAGCAAAG TTACTAAAAA ATACCACGAG GTCCTTCAGT

+3 L R P K T G V R G L H K S L T D V A L E
1021 TGAGACCAAA GACCGGTGTC AGGGGATTGC ACAAATCACT CACCGACGTG GCCCTGGAGC

+3 H H E E C D C V C R G S T G G
1081 accatgagga gtgtgactgt gtgtgcagag ggagcacagg aggatagctc taga

Fig. 20-2



VASCULAR ENDOTHELIAL GROWTH
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DNA AND POLYPEPTIDE SEQUENCE USED FOR E.coli EXPRESSION

```
+ 3   Q T N S S S N N N N N N N N N L G I
1   CGCAGACTAA TTCGAGCTCG AACAAACAACA ACAATAACAA TAACAACAAC CTCGGGATCG

      E G R I S E F E S N L S S K F Q F S S N
61  AGGGAAGGAT TTCAGAATTC GAATCCAACC TGAGTAGTAA ATTCCAGTTT TCCAGCAACA

+ 3   K E Q N G V Q D P Q H E R I I T V S T N
121 AGGAACAGAA CCGAGTACAA GATCCTCAGC ATGAGAGAAT TATTACTGTG TCTACTAATG

+ 3   G S I H S P R F P H T Y P R N T V L V W
181 GAAGTATTCA CAGCCCAAGG TTTCTCATA CTTATCCAAG AAqTACGGTC TTGGTATGGA

+ 3   R L V A V E E N V W I Q L T I D E R F G
241 GATTAGTXGC AGTAGAGGAA AATGTATGGA TACAACCTAC GTTTGATGAA AGATTTGGGC

+ 3   L E D P E D D I C K Y D F V E V E E P S
301 TTGAAGACCC AGAAGATGAC ATATGCAAGT ATGATTTTGT AGAAGTTGAG GAACCCAGTG

+ 3   D G T I L G R W C G S G T V P G K Q I S
361 ATGGAACTAT ATTAGGGCGC TGGTGTGGTT CTGGTACTGT ACCAGGAAAA CAGATTTCTA

+ 3   K G S Q I R I R F V S D E Y F P S E P G
421 AAGGAAATCA AATTAGGATA AGATTTGTAT CTGATGAATA TTTTCCTTCT GAACCAGGGT

+ 3   F C I H Y N I V M P Q F T E A V S P S V
481 TCTGCATCCA CTACAACATT GTCATGCCAC AATTCACAGA AGCTGTGAGT CCTTCAGTGC

+ 3   L P P S A L P L D L L N N A I T A F S T
541 TACCCCCTTC AGZTTTGCCA CTGGACCTGC TTAATAATGC TATAACTGCC TTAGTACCT

+ 3   L E D L I R Y L E P E R W Q L D L E D L
601 TGGAAGACCT TATTCGATAT CTTGAACCAG AGAGATGGCA GTTGACTTA GAAGATCTAT

+ 3   Y R P T W Q L L G K A F V F G R K S R V
661 ATAGGCCAAC TTGGCAACTT CTTGGCAAGG CTTTTGTTTT TGGAAGAAAA TCCAGAGTGG

+ 3   V D L N L L T E E V R L Y S C T P R N F
721 TGGATCCGAA CCTTCTAACA GAGGAGGTAA GATTATACAG CTGCACACCT CGTAACTTCT

+ 3   S V S I R E E L K R T D T I F W P G C L
781 CAGTGTCCAT AAGGGAAGAA CTAAAGAGAA CCGATACCAT TTTCTGGCCA GTTTGTCTCC
```

Fig. 21-1



VASCULAR ENDOTHELIAL GROWTH
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+ 3 L V K R C G G N C A C C L E N C N E C Q
841 TGGTTAAACG CTGCGGTGGG AACTGTGCCT GTTGTCTCCA CAATTGCAAT GAATGTCAAT

+ 3 C V I S K V T K K Y H E V L Q L R P K T
901 GTGTCCCAAG CAAAGTTACT AAAAAATACC ACGAGGTCCT TCAGTTGAGA CCAAAGACCG

+ 3 G V R G L H K S L T D V A L E H H E E C
961 GTGTCAGGGG ATTGCACAAA TCACTCACCG ACGTGGCCCT GGAGCACCAT GAGGAGTGTG

+ 3 D C V C R G S T G G H H H H H H *
1021 ACTGTGTGTG CAGAGGGAGC ACAGGAGGAC ATCATCACCA TCACCATTGA TCTAGAGTCG

1081 ACCTGCAGGC AAGCTT

Fig. 21-2

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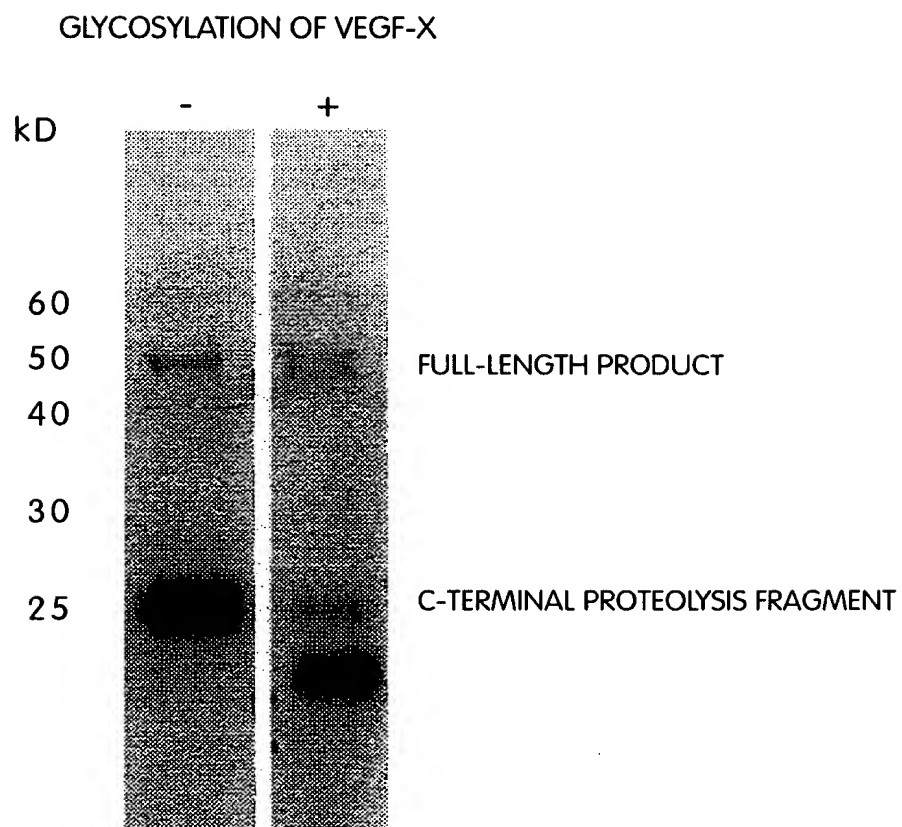


Fig. 23



VASCULAR ENDOTHELIAL GROWTH
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DNA AND POLYPEPTIDE SEQUENCE USED FOR E.coli
EXPRESSION OF THE PDGF-LIKE DOMAIN

```
+ 3           M R G S H H H H H H G M A S M
1  AAGGAGATAT ACATATGCGG GGTTCATC ATCATCATCA TCATGGTATG GCTAGCATGA

+ 3  T G G O O M G R D L Y D D D D K D P G R
61  CTGGTGGACA GCAAATGGGT CGGGATCTGT ACGACGATGA CGATAAGGAT CCGCGAAGAA

+ 3  K S R V V D L N L L T E E V R L Y S C T
121 AATCCAGAGT GGTGGATCTG AACCTTCTAA CAGAGGAGGT AAGATTATAC AGCTGCACAC

+ 3  P R N F S V S I R E E L K R T D T I F W
101 CTCGTAACCT CTCAGTGTCC ATAAGGGAAG AACTAAAGAG AACCGATACC ATTTTCTGGC

+ 3  P G C L L V K R C G G N C A C C L H N C
241 CAGGTTGTCT CCTGGTTAAA CGCTGTGGTG GGAAGTGTGC CTGTTGTCTC CACAATTGCA

+ 3  N E C Q C V P S K V T K K Y H E V L Q L
301 ATGAATGTCA ATGTGTCCCA AGCAAAGTTA CTAAAAAATA CCACGAGGTC CTTTCAGTTGA

+ 3  R P K T G V R G L H K S L T D V A L E H
361 GACCAAAGAC CCGTGTGAGG CGATTGCACA AATCACTCAC CGACGTGGCC CTGGAGCACC

+ 3  H E E C D C V C R G S T G G
421 ATGAGGAGTG TGAAGTGTG TGCAGAGGGA GCACAGGAGG ATAATGAATT CGAAGCTTGA

481 TCCGGCTGCT AACAAAGCCC
```

Fig. 24



VASCULAR ENDOTHELIAL GROWTH
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EXPRESSION OF PDGF DOMAIN IN E.coli

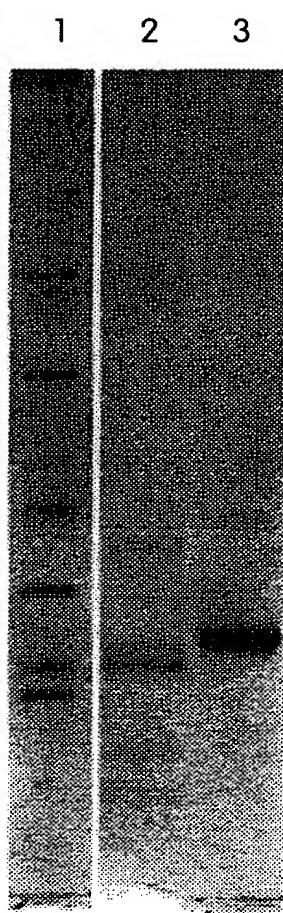
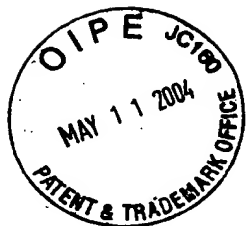


Fig. 25



VASCULAR ENDOTHELIAL GROWTH
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DNA AND POLYPEPTIDE SEQUENCE USED FOR E.coli
EXPRESSION OF THE CUB-LIKE DOMAIN

```
+ 2      M A M D I G I N S D P E S H H H H H H
1      GGCGATGGCC ATGGATATCG GAATTAATTC GGATCCGGAG TCTCACCATC ACCACCATCA

+2      E S N L S S K F Q F S S N K E Q N G V Q
61     TGAATCCAAC CTGAGTAGTA AATTCCAGTT TTCCAGCAAC AAGGAACAGA ACGGAGTACA

+2      D P Q H E R I I T V S T N G S I H S P R
121    AGATCCTCAG CATGAGAGAA TTATTACTGT GTCTACTAAT GGAAGTATTC ACAGCCCAAG

+2      F P H T Y P R N T V L V W R L V A V E E
181    GTTTCCTCAT ACTTATCCAA GAAATACGGT CTTGGTATGG AGATTAGTAG CAGTAGACGA

+2      N V W I Q L T F D E R F G L E D P E D D
241    AAATGTATGG ATACAACTTA CGTTTGATGA AAGATTTGGG CTTGAAGACC CAGAAGATGA

+ 2      I C K V D F V E V E E P S D G T I L G R
301    CATATGCAAG TATGATTTTG TAGAAGTTGA GGAACCCAGT GATGGAACTA TATTAGGGCG

+2      W C G S G T V P G K Q I S K G N Q I R I
361    CTGGTGTGGT TCTGGTACTG TACCAGGAAA ACAGATTTCT AAAGGAAATC AAATTAGGAT

+ 2      R F V S D E Y F P S E P G F C I H Y N I
421    AAGATTTGTA TCTGATGAAT ATTTTCCTTC TGAACCAGGG TTCTGCATCC ACTACAACAT

+2      V M P C F T E A V
491    TGTCATGCCA CAATTCACAG AAGCTGTGTA GTCGAGCTCC GTCGACAAGC TTGCGGCCGC

541    ACTCGAGCAC
```

Fig. 26



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EXPRESSION OF THE CUB DOMAIN IN E.coli

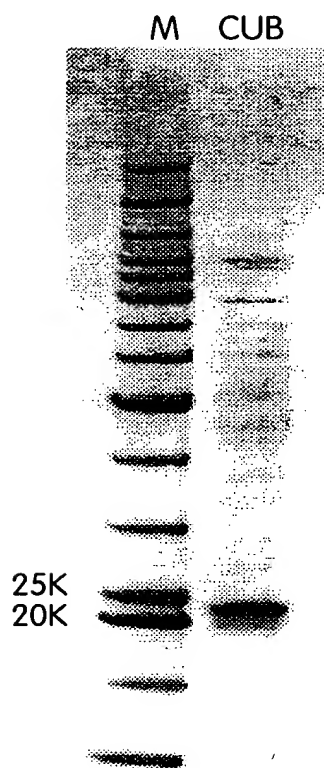


Fig. 27

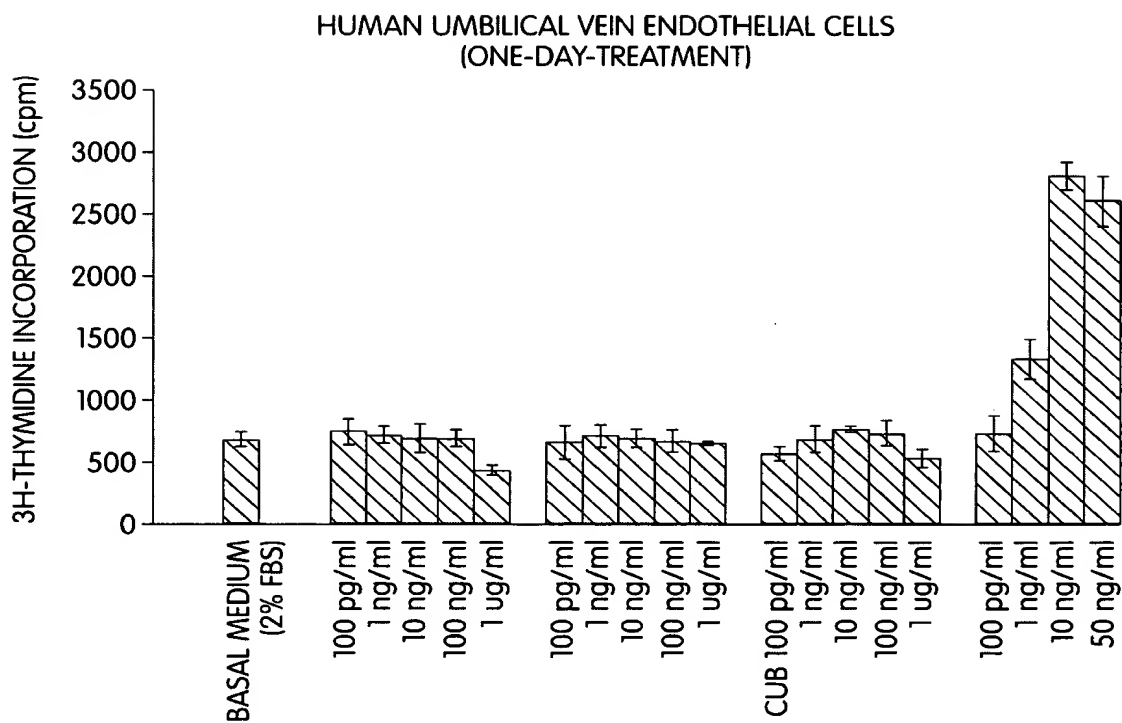


Fig. 28A



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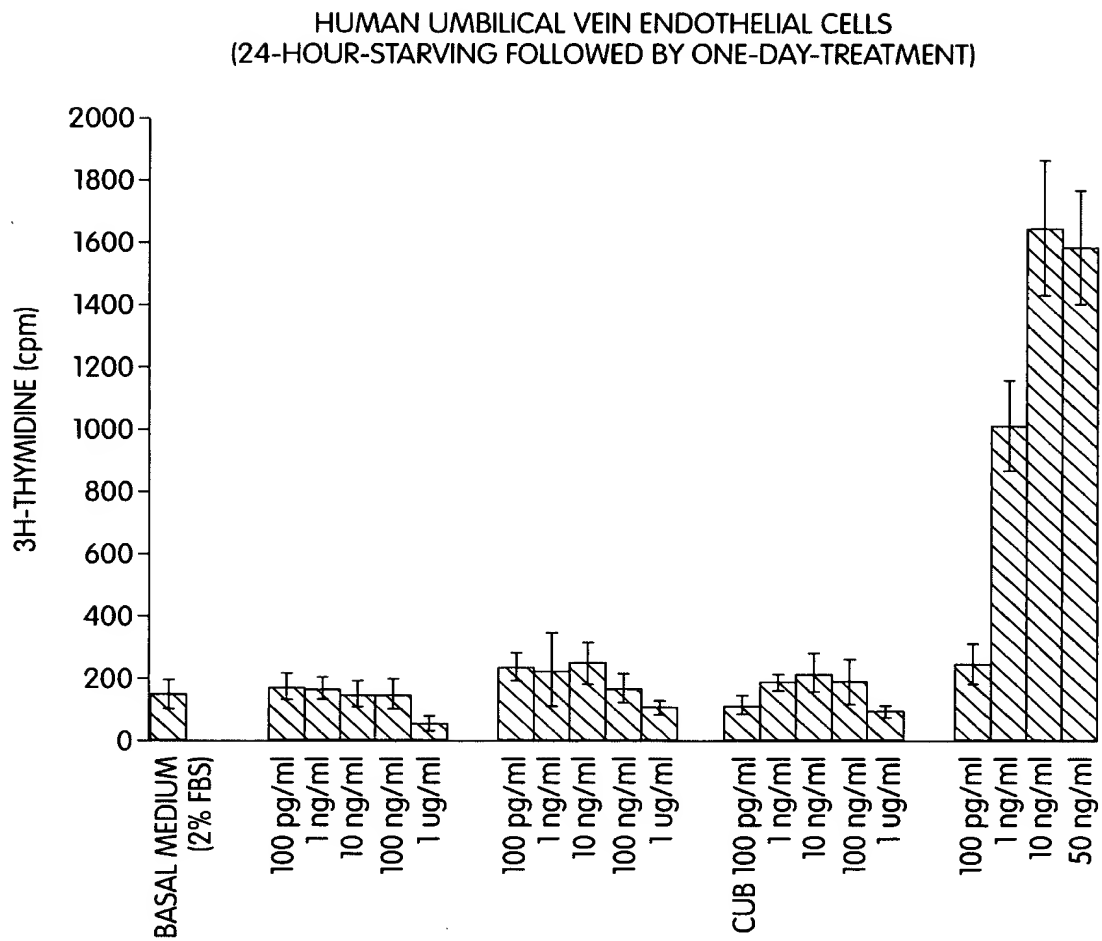


Fig. 28B



THE EFFECT OF VEGF-A₁₆₅ AND VEGF-X CUB DOMAIN
ON THE PROLIFERATION OF HUVEC (TWO-DAY-TREATMENT)

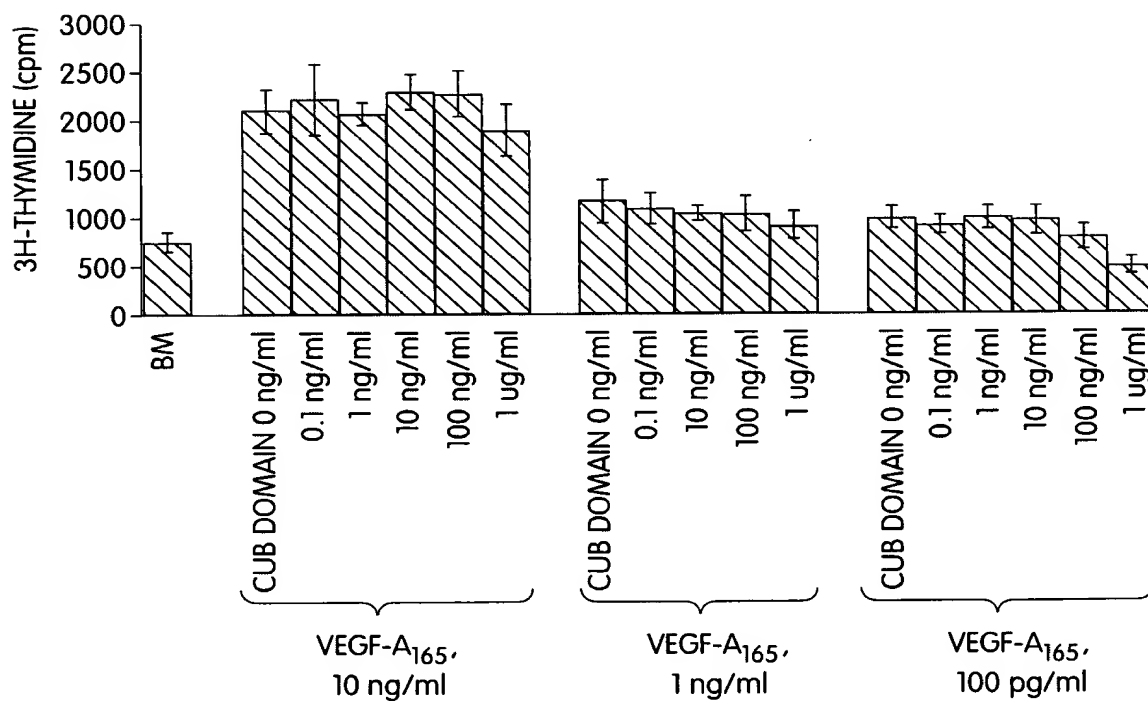


Fig. 28C



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NORMAL TISSUES

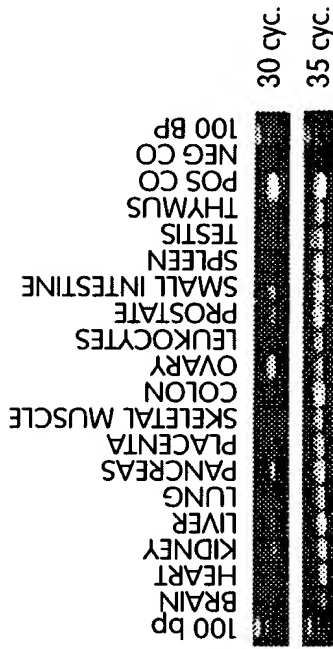
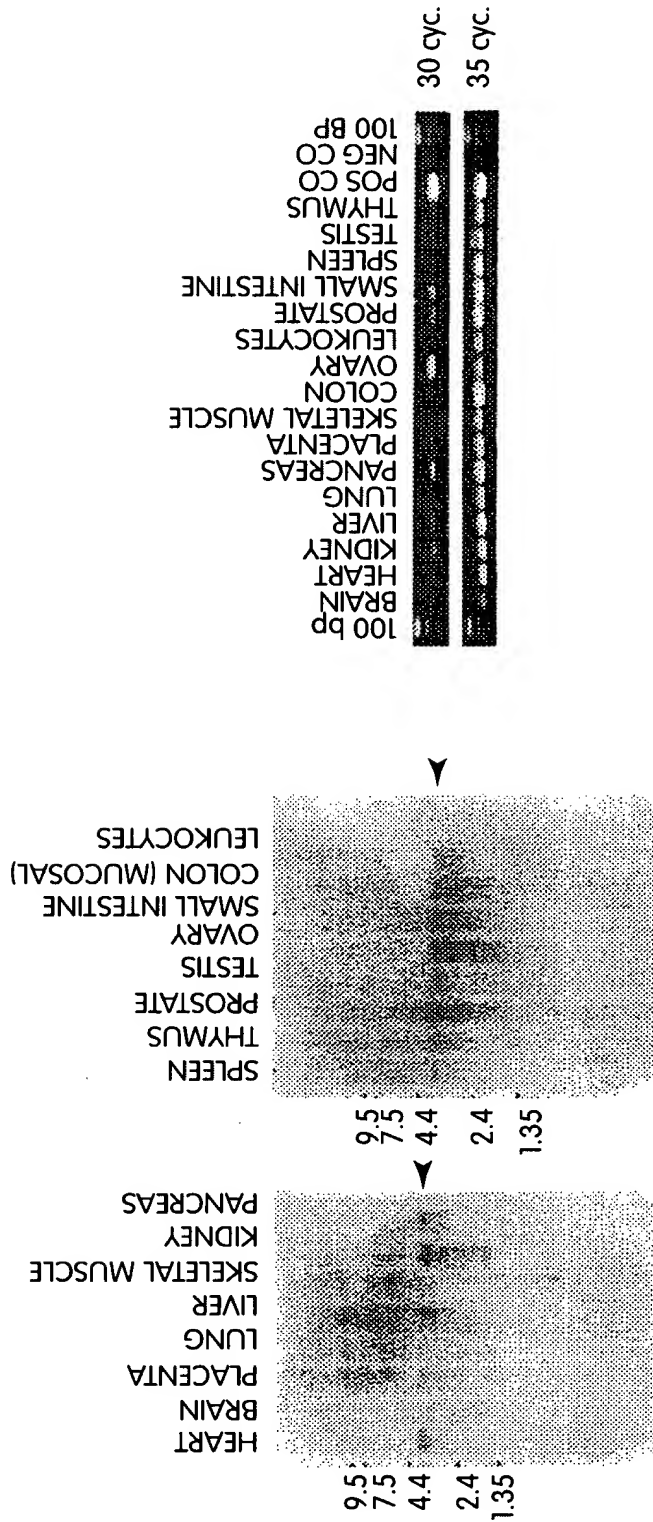


Fig. 29A



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TUMOR TISSUE AND CELL LINES

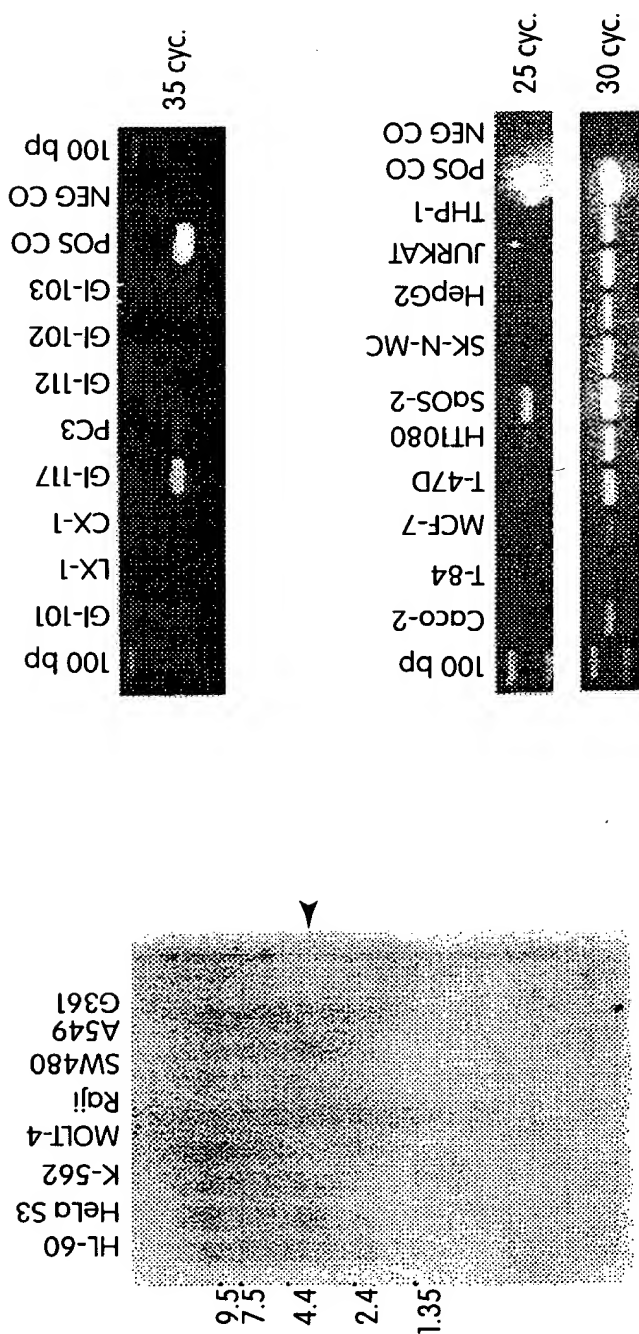


Fig. 29B



GENOMIC DNA SEQUENCES OF 2 EXONS DETERMINED BY SEQUENCING

tttcttttataccatatagtggtggatctgaaccagGGTTCTGCATCCACTACAACATTGTC
ATGCCACAATTCACAGAAGCTGTGAGTCCCTTCAGTGCTACCCCCTTCAGCTTTGCCACTGGA
CCTGCTTAATAATGCTATAACTGCCTTTAGTACCTTGGAAGACCTTATTCGATATCTTGAAC
CAGAGAGATGGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGAACCTTCTTGGCAAG
GCTTTTGT TTTTGGGAAGAAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGGAGGTAAG
ATTATACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCG
ATACCATTTTCTGGCCAGGTTGTCTCCTGGTTAAACGCTGTGGTGGGAACCTGTGCCTGTTGT
CTCCACAATTGCAATGAATGTCAATGTGTCCCAAGCAAAGTTACTAAAAAATACCACGAGgt
aggtatacaattttcttttttgggttctccttcgggtatttttatgtctt

aaagccagtcatagacattcgttgatttttaaaagtggcttactcttattcccttttcagGTC
CTTCAGTTGAGACCAAAGACCGGTGTGAGGGGATTGCACAAATCACTCACCGACGTGGCCCT
GGAGCACCATGAGGAGTGTGACTGTGTGTGCAGAGGGAGCACAGGAGGATAGCCGCATCACC
ACCAGCAGCTCTTGCCCAGAGCTGTGCAGTGCAGTGGCTGATTCTATTAGAGAACGTATGCG
TTATCTCCATCCTTAATCTCAGTTGTTTGCTTCAAGGACCTTTCATCTTCAGGATTTACAGT
GCATTCTGAAAGAGGAGACATCAAACAGAATTAGGAGTTGTGCAACAGCTCTTTTGAGAGGA
GGCCTAAAGGACAGGAGAAAAGGTCTTCAATCGTGGAAAGAAAATTAAATGTTGTATTAAAT
AGATCACCAGCTAGTTTCAGAGTTACCATGTACGTATTCCACTAGCTGGGTTCTGTATTTC
GTTCTTTTCGATACGGCTTAGGGTAATGTGAGTACAGGAAAAAACTGTGCAAGTGAGCACCT
GATTCCGTTGCCTTGGCTTAACTCTAAAGCTCCATGTCTGCGCCTAAATCGTATAAAAATC
TGGATTTTTTTTTTTTTTTTTTTTTCGCGCATATTCATATGTAAACCAGAACATTCATGTACTA
CAAACCTGGTTTTTTAAAAAGGAACATATGTTGCTATGAATTAACTTGTGTCATGCTGATAGG
ACAGACTGGATTTTTTCATATTTCTTATTAATAATTTCTGCCATTTAGAAGAAGAGAACTACAT
TCATGGTTTTGGAAGAGATAAACCTGAAAAGAAGAGTGGCCTTATCTTCACCTTTATCGATAAG
TCAGTTTATTTGTTTCATTGTGTACATTTTTTATATTCTCCTTTTGACATTATAACTGTTGGC
TTTTCTAATCTTGTTAAATATATCTATTTTTTACCAAAGGTATTTAATATTCTTTTTTTATGAC
AACTTAGATCAACTATTTTTTAGCTTGGTAAATTTTTCTAAACACAATTGTTATAGCCAGAGG
AACAAAGATGATATAAAATATTGTTGCTCTGACAAAAATACATGTATTTCACTCTCGTATGG
TGCTAGAGTTAGATTAATCTGCATTTTTAAAAAACTGAATTGGAATAGAATTGGTAAGTTGCA
AAGACTTTTTGAAAATAATTAAATTATCATATCTTCCATTCCTGTTATTGGAGATGAAAATA
AAAAGCAACTTATGAAAGTAGACATTGAGATCCAGCCATTACTAACCTATTCTTTTTTTGGG
GAAATCTGAGCCTAGCTCAGAAAAACATAAAGCACCTTGAAAAAGACTTGGCAGCTTCCTGA
TAAAGCGTGCTGTGCTGTGCAGTAGGAACACATCCTATTTATTGTGATGTTGTGGTTTTATT
ATCTTAAACTCTGTTCCATACACTTGTATAAATACATGGATATTTTTTATGTACAGAAGTATG
TCTCTTAACCAGTTCACTTATTGTACTCTGGCAATTTAAAAAGAAAATCAGTAAAAATATTTTG
CTTGTAATGCTTAATATCGTGCCTAGGTTATGTGGTGAATTTGAATCAAAAATGTATT
GAATCATCAATAAAAGAATGTGGCTATTTTGGGGAGAAAATTatgtgtgtgtgtgtgctcaag
atttatttcttggactctgagaaaatgaaagataaa

Fig. 30A



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LOCATION OF SPLICE SITES WITHIN THE cDNA SEQUENCE

1 GAATTCGCCC TTTTGTTTAA ACCTTGGGAA CTGGTTCAGG TCCAGGTTTT GCTTTGATCC
61 TTTTCAAAAA CTGGAGACAC AGAAGAGGGC TCTAGGAAAA AGTTTTGGAT GGGATTATGT
121 GGAAACTACC CTGCGATTCT CTGCTGCCAG AGCAGGCTCG GCGCTTCCAC CCCAGTGCAG
181 CCTTCCCCTG GCGGTGGTGA AAGAGACTCG GGAGTCGCTG CTTCCAAAGT GCCCCCCGTG
+3 M S L F G L L L L T S
241 AGTGAGCTCT CACCCCAGTC AGCCAAATGA GCCTCTTCGG GCTTCTCCTG CTGACATCTG
+3 A L A G Q R Q G T Q A E S N L S S K F Q
301 CCCTGGCCGG CCAGAGACAG GGGACTCAGG CGGAATCCAA CCTGAGTAGT AAATTCCAGT
+3 F S S N K E Q N G V Q D P Q H E R I I T
361 TTTCCAGCAA CAAGGAACAG AACGGAGTAC AAGATCCTCA GCATGAGAGA ATTATTACTG
+3 V S T N G S I H S P R F P H T Y P R N T
421 TGTCTACTAA TGGAAGTATT CACAGCCCAA GGTTCCTCA TACTTATCCA AGAAATACGG
+3 V L V W R L V A V E E N V W I Q L T F D
481 TCTTGGTATG GAGATTAGTA GCAGTAGAGG AAAATGTATG GATACAACCTT ACGTTTGATG
+3 E R F G L E D P E D D I C K Y D F V E V
541 AAAGATTTGG GCTTGAAGAC CCAGAAGATG ACATATGCAA GTATGATTTT GTAGAAGTTG
+3 E E P S D G T I L G R W C G S G T V P G
601 AGGAACCCAG TGATGGAACCT ATATTAGGGC GCTGGTGTGG TTCTGGTACT GTACCAGGAA
+3 K Q I S K G N Q I R I R F V S D E Y F P
661 AACAGATTTT TAAAGGAAAT CAAATTAGGA TAAGATTTGT ATCTGATGAA TATTTTCCTT
+3 S E P G F C I H Y N I V M P Q F T E A V
721 CTGAACCCAG GTTCTGCATC CACTACAACA TTGTCATGCC ACAATTCACA GAAGCTGTGA
+3 S P S V L P P S A L P L D L L N N A I T
781 GTCCTTCAGT GCTACCCCTC TCAGCTTTGC CACTGGACCT GCTTAATAAT GCTATAACTG
+3 A F S T L E D L I R Y L E P E R W Q L D
841 CCTTTAGTAC CTTGGAAGAC CTTATTCGAT ATCTTGAACC AGAGAGATGG CAGTTGGACT
+3 L E D L Y R P T W Q L L G K A F V F G R
901 TAGAAGATCT ATATAGGCCA ACTTGGCAAC TTCTTGGCAA GGCTTTTGTGTT TTTGGAAGAA
+3 K S R V V D L N L L T E E V R L Y S C T
961 AATCCAGAGT GGTGGATCTG AACCTTCTAA CAGAGGAGT AAGATTATAC AGCTGCACAC

Fig. 30B-1



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+3 P R N F S V S I R E E L K R T D T I F W
1021 CTCGTAAGTCT CTCAGTGTCC ATAAGGGAAG AACTAAAGAG AACCGATACC ATTTTCTGGC

+3 P G C L L V K R C G G N C A C C L H N C
1081 CAGGTTGTCT CCTGGTTAAA CGCTGTGGTG GGAAGTGTGC CTGTTGTCTC CACAATTGCA

+3 N E C Q C V P S K V T K K Y H E V L Q L
1141 ATGAATGTCA ATGTGTCCCA AGCAAAGTTA CTAAAAATA CCACGAGGTC CTTTCAGTTGA

+3 R P K T G V R G L H K S L T D V A L E H
1201 GACCAAAGAC CGGTGTCAGG GGATTGCACA AATCACTCAC CGACGTGGCC CTGGAGCACC

+3 H E E C D C V C R G S T G G
1261 ATGAGGAGTG TGACTGTGTG TGCAGAGGGA GCACAGGAGG ATAGCCGCAT CACCACCAGC

1321 AGCTCTTGCC CAGAGCTGTG CAGTGCAGTG GCTGATTCTA TTAGAGAACG TATGCGTTAT

1381 CTCCATCCTT AATCTCAGTT GTTTGCTTCA AGGACCTTTC ATCTTCAGGA TTTACAGTGC

1441 ATTCTGAAAG AGGAGACATC AAACAGAATT AGGAGTTGTG CAACAGCTCT TTTGAGAGGA

1501 GGCCTAAAGG ACAGGAGAAA AGGTCTTCAA TCGTGGAAAG AAAATTAAAT GTTGTATTAA

1561 ATAGATCACC AGCTAGTTTC AGAGTTACCA TGTACGTATT CCACTAGCTG GGTTCTGTAT

1621 TTCAGTTCTT TCGATACGGC TTAGGGTAAT GTCAGTACAG GAAAAAACT GTGCAAGTGA

1681 GCACCTGATT CCGTTGCCTT GCTTAACTCT AAAGCTCCAT GTCCTGGGCC TAAATCGTA

1741 TAAATCTGG ATTTTTTTTT TTTTTTTTGT CTCATATTCA CATATGTAAA CCAGAACATT

1801 CTATGTACTA CAAACCTGGT TTTTAAAAAG GAACTATGTT GCTATGAATT AAAGTTGTGT

1861 CATGCTGATA GGACAGACTG GATTTTTCAT ATTTCTTATT AAAATTTCTG CCATTTAGAA

1921 GAAGAGAACT ACATTCATGG TTTGGAAGAG ATAAACCTGA AAAGAAGAGT GGCCTTATCT

1981 TCACTTTATC GATAAGTCAG TTTATTTGTT TCATTGTGTA CATTTTATA TTCTCCTTTT

2041 GACATTATAA CTGTTGGCTT TTCTAATCTT GTTAAATATA TCTATTTTTA CCAAAGGTAT

2101 TTAATATTCT TTTTATGAC AACTTAGATC AACTATTTT AGCTTGGTAA ATTTTCTAA

2161 ACACAATTGT TATAGCCAGA GGAACAAAGA TGATATAAAA TATTGTTGCT CTGACAAAA

2221 TACATGTATT TCATTCTCGT ATGGTGCTAG AGTTAGATTA ATCTGCATTT TAAAAAACTG

2281 AATTGGAATA GAATTGGTAA GTTGCAAAGA CTTTTTGAAA ATAATTAAAT TATCATATCT

2341 TCCATTCCTG TTATTGGAGA TGAAAAATAA AAGCAACTTA TGAAAGTAGA CATTTCAGATC

2401 CAGCCATTAC TAACCTATTC CTTTTTTGGG GAAATCTGAG CCTAGCTCAG AAAACATAA

2461 AGCACCTTGA AAAAGACTTG GCAGCTTCCT GATAAAGCGT GCTGTGCTGT GCAGTAGGAA

2521 CACATCCTAT TTATTGTGAT GTTGTGGTTT TATTATCTTA AACTCTGTTC CATACTTGT

2581 TATAAATACA TGGATATTTT TATGTACAGA AGTATGTCTC TTAACCAGTT CACTTATTGT

2641 ACCTGGAAGG GCGAATTCTG CAGATATC

Fig. 30B-2



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THE EFFECT OF FL-VEGF-X ON HUVEC PROLIFERATION:
(24-HOUR SERUM STARVATION FOLLOWED BY ONE DAY-TREATMENT)

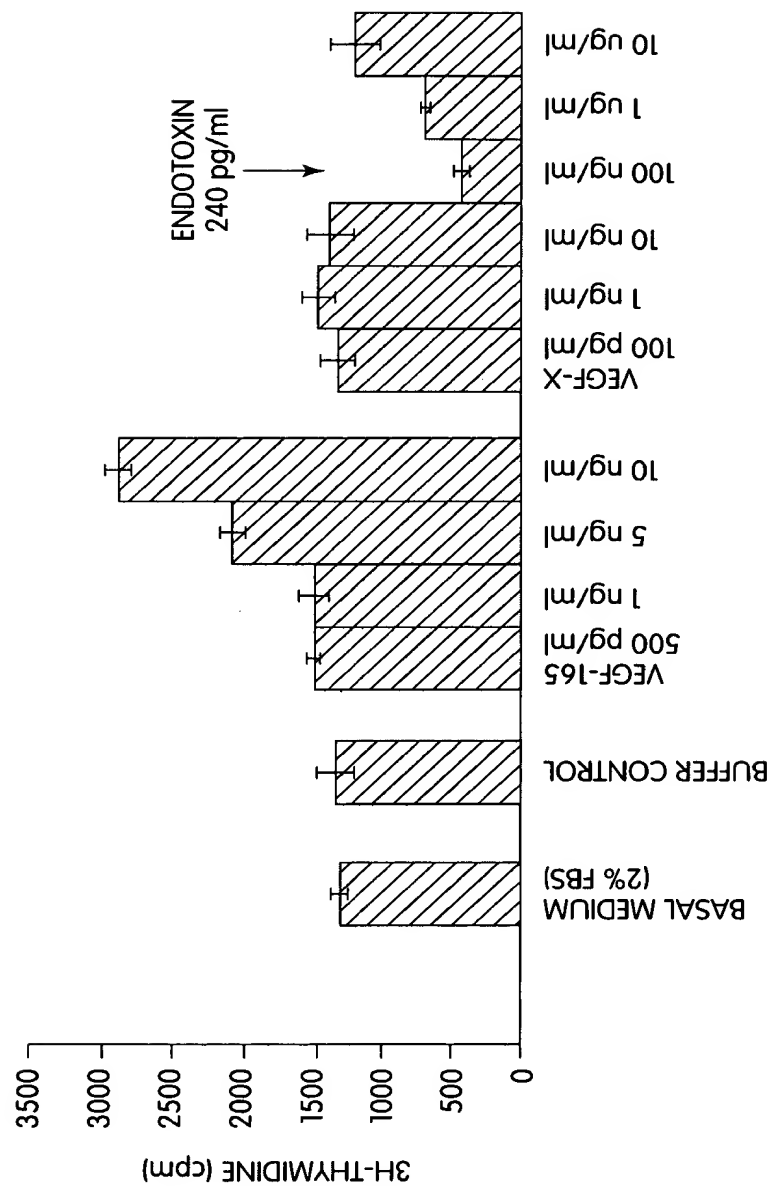


Fig. 31



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THE COMBINED EFFECT OF TRUNCATED VEGF-X (CUB DOMAIN) AND
HUMAN RECOMBINANT VEGF₁₆₅ ON HUVEC PROLIFERATION:
(24-HOUR SERUM STARVATION FOLLOWED BY TWO-DAY-TREATMENT)

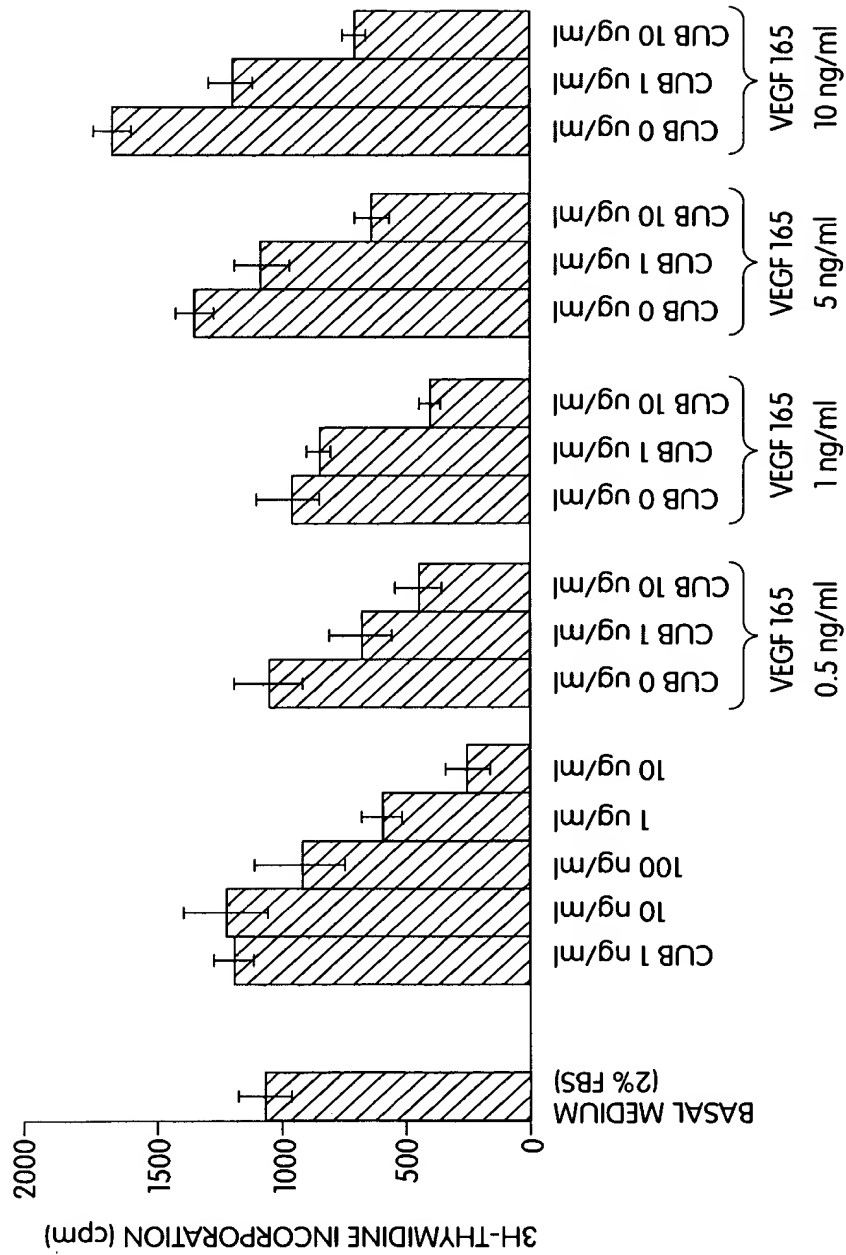


Fig. 32



THE COMBINED EFFECT OF CUB DOMAIN AND HUMAN RECOMBINANT
bFGF ON HUVEC PROLIFERATION:
(24-HOUR SERUM STARVATION FOLLOWED BY TWO-DAY-TREATMENT)

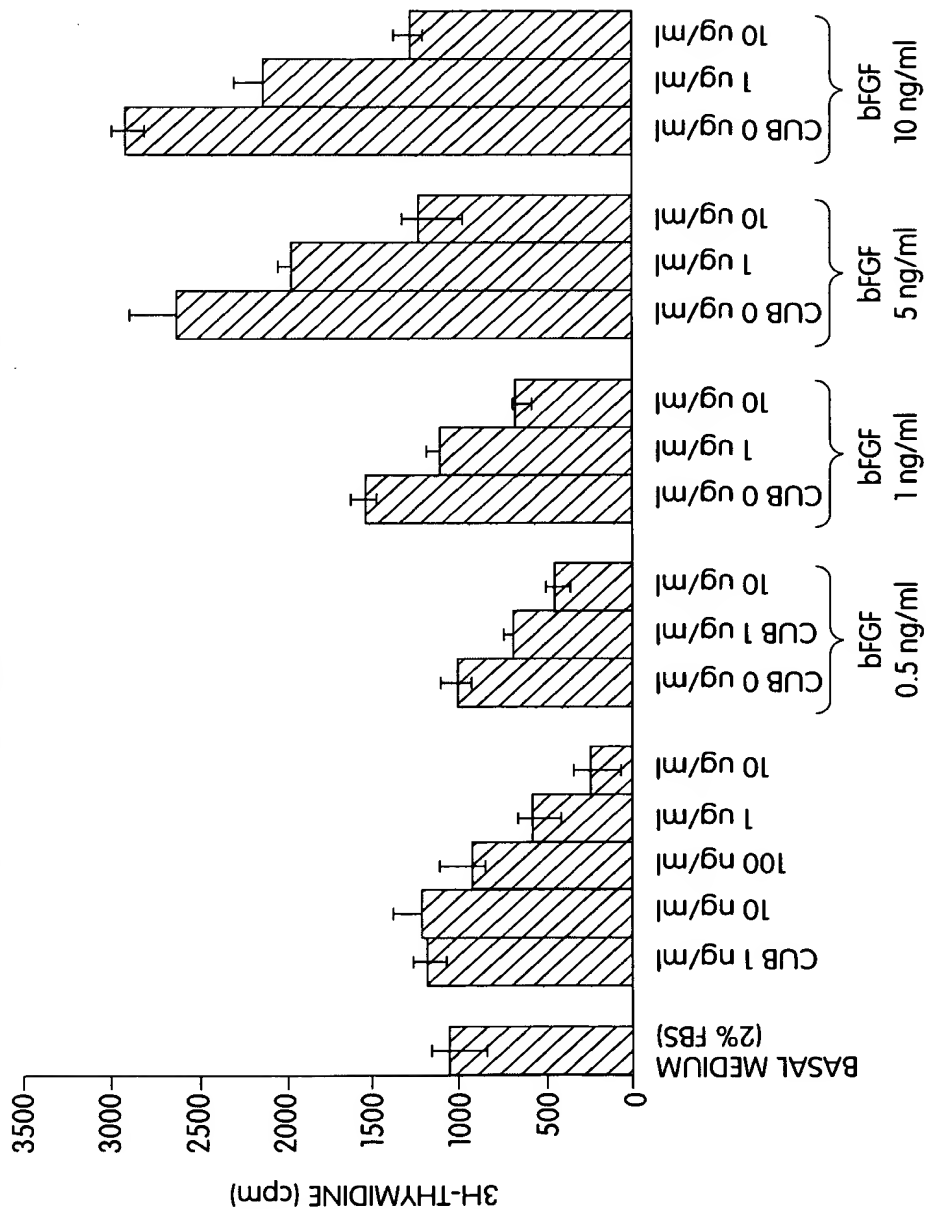


Fig. 33

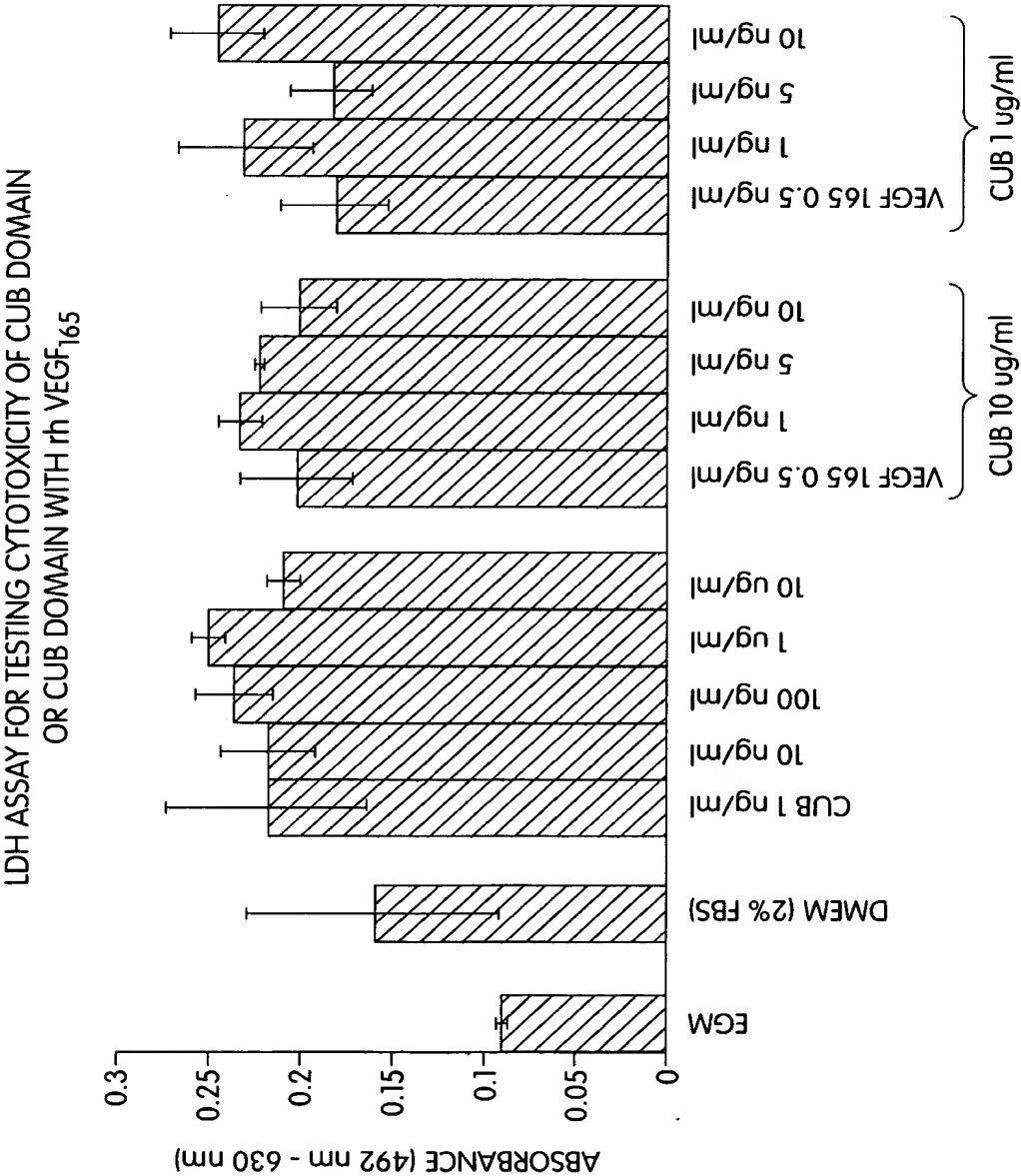


Fig. 34



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LDH ASSAY FOR TESTING CYTOTOXICITY OF CUB DOMAIN
OR CUB DOMAIN WITH rh-bFGF

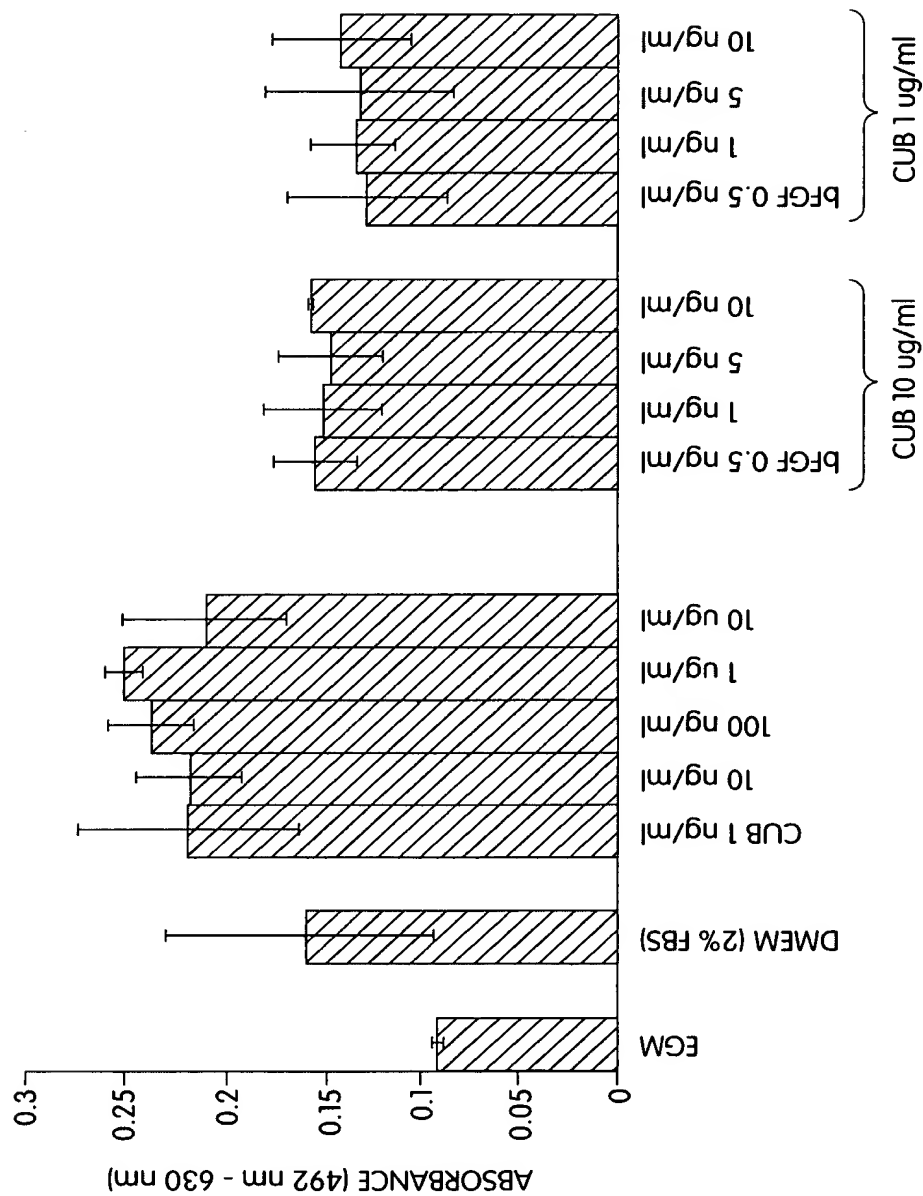


Fig. 35